



49321-142 SEQ LIST.txt
SEQUENCE LISTING

<110> MOSES, Ashlee
Frueh, Klaus
King, Jeffrey S.
Hicks, James B.
Raggo, Camilo
Nelson, Jay

<120> METHODS OF TREATMENT AND DIAGNOSIS OF KAPOSI'S SARCOMA (KS) AND
KS RELATED DISEASES

<130> 49321-142

<140> US 10/541,598
<141> 2005-07-05

<150> US 60/438,343
<151> 2003-01-06

<150> US 60/473,246
<151> 2003-05-22

<150> PCT US04/00320
<151> 2004-01-06

<160> 33

<170> PatentIn version 3.3

<210> 1
<211> 2035
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (152)..(1240)

<400> 1
tgcaagtctg cagccagcag agctcacagt tgttgcaaag tgctcagcac taagggagcc 60
agcgcacagc acagccagga aggcgagcga gcccagccag cccagccagc ccagccagcc 120
cggaggtcat ttgattgccc gcctcagaac g atg gat ctg cat ctc ttc gac 172
Met Asp Leu His Leu Phe Asp
1 5
tac tca gag cca ggg aac ttc tcg gac atc agc tgg cca tgc aac agc 220
Tyr Ser Glu Pro Gly Asn Phe Ser Asp Ile Ser Trp Pro Cys Asn Ser
10 15 20
agc gac tgc atc gtg gtg gac acg gtg atg tgt ccc aac atg ccc aac 268
Ser Asp Cys Ile Val Val Asp Thr Val Met Cys Pro Asn Met Pro Asn
25 30 35
aaa agc gtc ctg ctc tac acg ctc tcc ttc att tac att ttc atc ttc 316
Lys Ser Val Leu Leu Tyr Thr Leu Ser Phe Ile Tyr Ile Phe Ile Phe

49321-142 SEQ LIST.txt

40	45	50	55	
gtc atc ggc atg att gcc aac tcc gtg gtg gtc tgg gtg aat atc cag				364
Val Ile Gly Met Ile Ala Asn Ser Val Val Val Trp Val Asn Ile Gln	60	65	70	
gcc aag acc aca ggc tat gac acg cac tgc tac atc ttg aac ctg gcc				412
Ala Lys Thr Thr Gly Tyr Asp Thr His Cys Tyr Ile Leu Asn Leu Ala	75	80	85	
att gcc gac ctg tgg gtt gtc ctc acc atc cca gtc tgg gtg gtc agt				460
Ile Ala Asp Leu Trp Val Val Leu Thr Ile Pro Val Trp Val Val Ser	90	95	100	
ctc gtg cag cac aac cag tgg ccc atg ggc gag ctc acg tgc aaa gtc				508
Leu Val Gln His Asn Gln Trp Pro Met Gly Glu Leu Thr Cys Lys Val	105	110	115	
aca cac ctc atc ttc tcc atc aac ctc ttc ggc agc att ttc ttc ctc				556
Thr His Leu Ile Phe Ser Ile Asn Leu Phe Gly Ser Ile Phe Phe Leu	120	125	130	135
acg tgc atg agc gtg gac cgc tac ctc tcc atc acc tac ttc acc aac				604
Thr Cys Met Ser Val Asp Arg Tyr Leu Ser Ile Thr Tyr Phe Thr Asn	140	145	150	
acc ccc agc agc agg aag aag atg gta cgc cgt gtc gtc tgc atc ctg				652
Thr Pro Ser Ser Arg Lys Lys Met Val Arg Arg Val Val Cys Ile Leu	155	160	165	
gtg tgg ctg ctg gcc ttc tgc gtg tct ctg cct gac acc tac tac ctg				700
Val Trp Leu Leu Ala Phe Cys Val Ser Leu Pro Asp Thr Tyr Tyr Leu	170	175	180	
aag acc gtc acg tct gcg tcc aac aat gag acc tac tgc cgg tcc ttc				748
Lys Thr Val Thr Ser Ala Ser Asn Asn Glu Thr Tyr Cys Arg Ser Phe	185	190	195	
tac ccc gag cac agc atc aag gag tgg ctg atc ggc atg gag ctg gtc				796
Tyr Pro Glu His Ser Ile Lys Glu Trp Leu Ile Gly Met Glu Leu Val	200	205	210	215
tcc gtt gtc ttg ggc ttt gcc gtt ccc ttc tcc att atc gct gtc ttc				844
Ser Val Val Leu Gly Phe Ala Val Pro Phe Ser Ile Ile Ala Val Phe	220	225	230	
tac ttc ctg ctg gcc aga gcc atc tcg gcg tcc agt gac cag gag aag				892
Tyr Phe Leu Leu Ala Arg Ala Ile Ser Ala Ser Ser Asp Gln Glu Lys	235	240	245	
cac agc agc cgg aag atc atc ttc tcc tac gtg gtg gtc ttc ctt gtc				940
His Ser Ser Arg Lys Ile Ile Phe Ser Tyr Val Val Val Phe Leu Val	250	255	260	
tgc tgg ctg ccc tac cac gtg gcg gtg ctg ctg gac atc ttc tcc atc				988
Cys Trp Leu Pro Tyr His Val Ala Val Leu Leu Asp Ile Phe Ser Ile	265	270	275	
ctg cac tac atc cct ttc acc tgc cgg ctg gag cac gcc ctc ttc acg				1036

49321-142 SEQ LIST.txt

Leu His Tyr Ile Pro Phe Thr Cys Arg Leu Glu His Ala Leu Phe Thr	
280 285 290 295	
gcc ctg cat gtc aca cag tgc ctg tcg ctg gtg cac tgc tgc gtc aac	1084
Ala Leu His Val Thr Gln Cys Leu Ser Leu Val His Cys Cys Val Asn	
300 305 310	
cct gtc ctc tac agc ttc atc aat cgc aac tac agg tac gag ctg atg	1132
Pro Val Leu Tyr Ser Phe Ile Asn Arg Asn Tyr Arg Tyr Glu Leu Met	
315 320 325	
aag gcc ttc atc ttc aag tac tcg gcc aaa aca ggg ctc acc aag ctc	1180
Lys Ala Phe Ile Phe Lys Tyr Ser Ala Lys Thr Gly Leu Thr Lys Leu	
330 335 340	
atc gat gcc tcc aga gtc tca gag acg gag tac tct gcc ttg gag cag	1228
Ile Asp Ala Ser Arg Val Ser Glu Thr Glu Tyr Ser Ala Leu Glu Gln	
345 350 355	
agc acc aaa tga tctgccctgg agaggctctg ggacggggtt acttggtttt	1280
Ser Thr Lys	
360	
gaacaggggtg atgggcccta tggttttcta gagcaaagca aagtagcttc gggctcttgat	1340
gcttgagtag agtgaagagg ggagcacgtg cccctgcat ccattctctc tttctcttga	1400
tgacgcagct gtcatttggc tgtgcgtgct gacagttttg caacaggcag agctgtgtcg	1460
cacagcagtg ctgtgcgtca gagccagctg aggacaggct tgccctggact tctgtaagat	1520
aggattttct gtgtttcctg aattttttat atgggtgattt gtattttaa atttaagactt	1580
tattttctca ctattggtgt accttataaa tgtatttgaa agttaaatat attttaaata	1640
ttgtttggga ggcatagtgc tgacatatat tcagagtgtt gtagttttta ggttagcgtg	1700
acttcagttt tgactaagga tgacactaat tgttagctgt tttgaaatta tatatatata	1760
aatatatata aatatataaa tatatgccag tcttggtgta aatgttttat ttaccatagt	1820
tttatatctg tgtggtgttt tgtaccggca cgggatatgg aacgaaaact gctttgtaat	1880
gcagtttgtg acattaatag tattgtaaag ttacatttta aaataaacia aaaactgttc	1940
tggaactgcaa atctgcacac acaacgaaca gttgcatttc agagagttct ctcaatttgt	2000
aagttatttt tttttaataa agatttttgt ttcct	2035

<210> 2
 <211> 362
 <212> PRT
 <213> homo sapiens
 <400> 2

Met Asp Leu His Leu Phe Asp Tyr Ser Glu Pro Gly Asn Phe Ser Asp
1 5 10 15

49321-142 SEQ LIST.txt

Ile Ser Trp Pro Cys Asn Ser Ser Asp Cys Ile Val Val Asp Thr Val
20 25 30

Met Cys Pro Asn Met Pro Asn Lys Ser Val Leu Leu Tyr Thr Leu Ser
35 40 45

Phe Ile Tyr Ile Phe Ile Phe Val Ile Gly Met Ile Ala Asn Ser Val
50 55 60

Val Val Trp Val Asn Ile Gln Ala Lys Thr Thr Gly Tyr Asp Thr His
65 70 75 80

Cys Tyr Ile Leu Asn Leu Ala Ile Ala Asp Leu Trp Val Val Leu Thr
85 90 95

Ile Pro Val Trp Val Val Ser Leu Val Gln His Asn Gln Trp Pro Met
100 105 110

Gly Glu Leu Thr Cys Lys Val Thr His Leu Ile Phe Ser Ile Asn Leu
115 120 125

Phe Gly Ser Ile Phe Phe Leu Thr Cys Met Ser Val Asp Arg Tyr Leu
130 135 140

Ser Ile Thr Tyr Phe Thr Asn Thr Pro Ser Ser Arg Lys Lys Met Val
145 150 155 160

Arg Arg Val Val Cys Ile Leu Val Trp Leu Leu Ala Phe Cys Val Ser
165 170 175

Leu Pro Asp Thr Tyr Tyr Leu Lys Thr Val Thr Ser Ala Ser Asn Asn
180 185 190

Glu Thr Tyr Cys Arg Ser Phe Tyr Pro Glu His Ser Ile Lys Glu Trp
195 200 205

Leu Ile Gly Met Glu Leu Val Ser Val Val Leu Gly Phe Ala Val Pro
210 215 220

Phe Ser Ile Ile Ala Val Phe Tyr Phe Leu Leu Ala Arg Ala Ile Ser
225 230 235 240

Ala Ser Ser Asp Gln Glu Lys His Ser Ser Arg Lys Ile Ile Phe Ser

49321-142 SEQ LIST.txt

245

250

255

Tyr Val Val Val Phe Leu Val Cys Trp Leu Pro Tyr His Val Ala Val
 260 265 270

Leu Leu Asp Ile Phe Ser Ile Leu His Tyr Ile Pro Phe Thr Cys Arg
 275 280 285

Leu Glu His Ala Leu Phe Thr Ala Leu His Val Thr Gln Cys Leu Ser
 290 295 300

Leu Val His Cys Cys Val Asn Pro Val Leu Tyr Ser Phe Ile Asn Arg
 305 310 315 320

Asn Tyr Arg Tyr Glu Leu Met Lys Ala Phe Ile Phe Lys Tyr Ser Ala
 325 330 335

Lys Thr Gly Leu Thr Lys Leu Ile Asp Ala Ser Arg Val Ser Glu Thr
 340 345 350

Glu Tyr Ser Ala Leu Glu Gln Ser Thr Lys
 355 360

<210> 3
 <211> 1421
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (115)..(1092)

<400> 3
 ggcgagggag gaggaagaag cggaggaggc ggctcccgcg ctcgcagggc cgtgccacct 60

gcccgcgccgc ccgctcgctc gctcgcccgc cgcgccgcgc tgccgaccgc cagc atg 117
 Met
 1

ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg ccg ccg ctg 165
 Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Pro Leu
 5 10 15

ctg ccg ctg ctg ctg ctg cta ctg ggc gcg agt ggc ggc ggc ggc ggc 213
 Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Ser Gly Gly Gly Gly Gly
 20 25 30

gcg cgc gcg gag gtg ctg ttc cgc tgc ccg ccc tgc aca ccc gag cgc 261
 Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys Thr Pro Glu Arg
 35 40 45

49321-142 SEQ LIST.txt

ctg gcc gcc tgc ggg ccc ccg ccg gtt gcg ccg ccc gcc gcg gtg gcc Leu Ala Ala Cys Gly Pro Pro Pro Val Ala Pro Pro Ala Ala Val Ala 50 55 60 65	309
gca gtg gcc gga ggc gcc cgc atg cca tgc gcg gag ctc gtc cgg gag Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu Leu Val Arg Glu 70 75 80	357
ccg ggc tgc ggc tgc tgc tcg gtg tgc gcc cgg ctg gag ggc gag gcg Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu Glu Gly Glu Ala 85 90 95	405
tgc ggc gtc tac acc ccg cgc tgc ggc cag ggg ctg cgc tgc tat ccc Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu Arg Cys Tyr Pro 100 105 110	453
cac ccg ggc tcc gag ctg ccc ctg cag gcg ctg gtc atg ggc gag ggc His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val Met Gly Glu Gly 115 120 125	501
act tgt gag aag cgc cgg gac gcc gag tat ggc gcc agc ccg gag cag Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala Ser Pro Glu Gln 130 135 140 145	549
gtt gca gac aat ggc gat gac cac tca gaa gga ggc ctg gtg gag aac Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly Leu Val Glu Asn 150 155 160	597
cac gtg gac agc acc atg aac atg ttg ggc ggg gga ggc agt gct ggc His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly Gly Ser Ala Gly 165 170 175	645
cgg aag ccc ctc aag tcg ggt atg aag gag ctg gcc gtg ttc cgg gag Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala Val Phe Arg Glu 180 185 190	693
aag gtc act gag cag cac cgg cag atg ggc aag ggt ggc aag cat cac Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly Gly Lys His His 195 200 205	741
ctt ggc ctg gag gag ccc aag aag ctg cga cca ccc cct gcc agg act Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro Pro Ala Arg Thr 210 215 220 225	789
ccc tgc caa cag gaa ctg gac cag gtc ctg gag cgg atc tcc acc atg Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg Ile Ser Thr Met 230 235 240	837
cgc ctt ccg gat gag cgg ggc cct ctg gag cac ctc tac tcc ctg cac Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu Tyr Ser Leu His 245 250 255	885
atc ccc aac tgt gac aag cat ggc ctg tac aac ctc aaa cag tgc aag Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu Lys Gln Cys Lys 260 265 270	933
atg tct ctg aac ggg cag cgt ggg gag tgc tgg tgt gtg aac ccc aac Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys Val Asn Pro Asn	981

49321-142 SEQ LIST.txt

275

280

285

acc ggg aag ctg atc cag gga gcc ccc acc atc cgg ggg gac ccc gag 1029
 Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly Asp Pro Glu
 290 295 300 305

tgt cat ctc ttc tac aat gag cag cag gag gct cgc ggg gtg cac acc 1077
 Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Arg Gly Val His Thr
 310 315 320

cag cgg atg cag tag accgcagcca gccgggtgcct ggcgcccctg cccccgccc 1132
 Gln Arg Met Gln
 325

ctctccaaac accggcagaa aacggagagt gcttgggtgg tgggtgctgg aggattttcc 1192

agttctgaca cacgtattta tatttggaag gagaccagca ccgagctcgg cacctccccg 1252

gcctctctct tcccagctgc agatgccaca cctgctcctt cttgctttcc ccgggggagg 1312

aaggggggttg tggtcgggga gctgggggtac aggtttgggg agggggaaga gaaattttta 1372

tttttgaacc cctgtgtccc ttttgcataa gattaaagga aggaaaagt 1421

<210> 4

<211> 325

<212> PRT

<213> homo sapiens

<400> 4

Met Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Pro
 1 5 10 15

Leu Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Ser Gly Gly Gly Gly
 20 25 30

Gly Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys Thr Pro Glu
 35 40 45

Arg Leu Ala Ala Cys Gly Pro Pro Pro Val Ala Pro Pro Ala Ala Val
 50 55 60

Ala Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu Leu Val Arg
 65 70 75 80

Glu Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu Glu Gly Glu
 85 90 95

Ala Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu Arg Cys Tyr
 100 105 110

49321-142 SEQ LIST.txt

Pro His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val Met Gly Glu
115 120 125

Gly Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala Ser Pro Glu
130 135 140

Gln Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly Leu Val Glu
145 150 155 160

Asn His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly Gly Ser Ala
165 170 175

Gly Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala Val Phe Arg
180 185 190

Glu Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly Gly Lys His
195 200 205

His Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro Pro Ala Arg
210 215 220

Thr Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg Ile Ser Thr
225 230 235 240

Met Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu Tyr Ser Leu
245 250 255

His Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu Lys Gln Cys
260 265 270

Lys Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys Val Asn Pro
275 280 285

Asn Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly Asp Pro
290 295 300

Glu Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Arg Gly Val His
305 310 315 320

Thr Gln Arg Met Gln
325

<210> 5

<211> 2502

49321-142 SEQ LIST.txt

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (76)..(624)

<400> 5

```

ctcttttgccc aagccctgcc tctgtacagc ctcgagtggc cagccagagg ctgcagctgg      60

agccccagagc ccaag atg gag ccc cag ctg ggg cct gag gct gcc gcc ctc      111
      Met Glu Pro Gln Leu Gly Pro Glu Ala Ala Ala Leu
              1              5              10

cgc cct ggc tgg ctg gcc ctg ctg ctg tgg gtc tca gcc ctg agc tgt      159
Arg Pro Gly Trp Leu Ala Leu Leu Leu Trp Val Ser Ala Leu Ser Cys
      15              20              25

tct ttc tcc ttg cca gct tct tcc ctt tct tct ctg gtg ccc caa gtc      207
Ser Phe Ser Leu Pro Ala Ser Ser Leu Ser Ser Leu Val Pro Gln Val
      30              35              40

aga acc agc tac aat ttt gga agg act ttc ctc ggt ctt gat aaa tgc      255
Arg Thr Ser Tyr Asn Phe Gly Arg Thr Phe Leu Gly Leu Asp Lys Cys
      45              50              55              60

aat gcc tgc atc ggg aca tct att tgc aag aag ttc ttt aaa gaa gaa      303
Asn Ala Cys Ile Gly Thr Ser Ile Cys Lys Lys Phe Phe Lys Glu Glu
      65              70              75

ata aga tct gac aac tgg ctg gct tcc cac ctt gga ctg cct ccc gat      351
Ile Arg Ser Asp Asn Trp Leu Ala Ser His Leu Gly Leu Pro Pro Asp
      80              85              90

tcc ttg ctt tct tat cct gca aat tac tca gat gat tcc aaa atc tgg      399
Ser Leu Leu Ser Tyr Pro Ala Asn Tyr Ser Asp Asp Ser Lys Ile Trp
      95              100              105

cgc cct gtg gag atc ttt aga ctg gtc agc aaa tat caa aac gag atc      447
Arg Pro Val Glu Ile Phe Arg Leu Val Ser Lys Tyr Gln Asn Glu Ile
      110              115              120

tca gac agg aaa atc tgt gcc tct gca tca gcc cca aag acc tgc agc      495
Ser Asp Arg Lys Ile Cys Ala Ser Ala Ser Ala Pro Lys Thr Cys Ser
      125              130              135              140

att gag cgt gtc ctg cgg aaa aca gag agg ttc cag aaa tgg ctg cag      543
Ile Glu Arg Val Leu Arg Lys Thr Glu Arg Phe Gln Lys Trp Leu Gln
      145              150              155

gcc aag cgc ctc acg ccg gac ctg gtg cag gac tgt cac cag ggc cag      591
Ala Lys Arg Leu Thr Pro Asp Leu Val Gln Asp Cys His Gln Gly Gln
      160              165              170

aga gaa cta aag ttc ctg tgt atg ctg aga taa caccagtga aaagcctggc      644
Arg Glu Leu Lys Phe Leu Cys Met Leu Arg
      175              180

```

49321-142 SEQ LIST.txt

atggagccca	gcactgagaa	cttccagaaa	gtgttagcct	tctcccaact	gtgttatacc	704
aaccacattt	tcaaatagta	atcattaaag	aggcttctgc	atcaaaccct	cacatgcagc	764
tcccatgcc	ccctccagaa	ttcaccaaca	cacaggccca	ccagcaacag	gctacctttg	824
cacaatatc	tctgatgaca	actccaaagc	cccggctctt	tccaccacac	tgtgggtcccc	884
tagatggggc	tggtgctgag	cccaccccaa	tccagatgtg	atccccctgt	gatctacttc	944
tggaagatt	ctcagtctgg	acaggtcttc	cctatgagat	agaacctgat	aaggagctag	1004
ggcaattctg	acaacattac	caaaggccca	cataacttct	aaatttttgt	ctgggtctgaa	1064
ggaaaacctg	ttctcgccct	agtgatggat	gaactctctt	atctctggct	tctagagggga	1124
aaaaaaaagc	atacctcttt	tactttttta	gtacctccat	cagagtcatg	aaatcacctg	1184
tcaagactat	ctatctttta	tgtttccatt	ctggtaagaa	ctcttttaaat	gaggacactg	1244
ctgattgctg	gtgatgtttt	ttgagcaaac	actcgggggt	atggatgaaa	gccaatcgca	1304
ggtcaaatga	ctccttgggg	aagctacttc	tcctctattc	agatttcact	aaaatcttcc	1364
aagatgaaag	caaactctaga	tttcggtctt	cattgctgtc	cattttttgta	atgaacgagt	1424
gtttttcctt	tagctagtgt	atcaggcagg	gttctaccag	agaaacagaa	ccagtaggag	1484
atacatatac	atgtccagat	ttatttcaaa	gaattgattt	acatgattgt	ggggattggc	1544
aagtccaaaa	tccatatggg	aggcctgcaa	tctgtaaacc	tttgggcagg	agctgatgct	1604
gtagtttgca	gatagaattc	cttggttcctt	aaaaaaatct	gtttttgttc	ttaagggtct	1664
tgaatgattg	gatcaggccc	accagatta	cctagataat	ctcttttact	taaagtaaac	1724
tgattgtagg	tgctaatac	atctatgaaa	tgccttcaca	gcaacaccta	gattagcatt	1784
caattgaata	actggggaat	acagcctagc	caagttgaca	cataaaatta	accatcacag	1844
caacatgcct	gctaaatttt	atcgaccgtc	ttcagactgt	taaggattgt	ggtagagaac	1904
tgtgacagcc	actctcagca	tcaccctgaa	ccaaaggccc	ctatcaagta	acaatatagc	1964
caagcaaaat	tccagtcaat	agagacattg	actggttggc	tggcttccca	agggatagca	2024
ccagacaaga	aatgcaagga	tgaggaaacc	aggcacggga	gaggaggagg	caacagagggt	2084
ccagggtttg	gttatctttt	tattttttcac	tgggaggtgg	taagttagcc	ctgttgccca	2144
tgtatgcaga	tgggagaagt	gatttagaaa	ctccaaagca	attggtaatc	cccaaaatgg	2204
gtgtatctgg	tttgaaatga	aaccttat	tattggaaat	ggttggtttc	ccaattctgt	2264
ttgccattgg	ccaatataat	tgtgggtttg	cacatggcca	gcacatgcc	aacagaagta	2324
gacaaaggtc	tcactctgta	agtgggacct	tggggaggag	ctgcctccat	cataaagggga	2384
gggggttagta	aaaatgggtct	cttaagcctg	ttcctgctac	agttatagag	gttgctcaga	2444

49321-142 SEQ LIST.txt

accttctcag caaatatagc agttatctat tgttgtgtat taaaccattt caacacat 2502

<210> 6
<211> 182
<212> PRT
<213> homo sapiens

<400> 6

Met Glu Pro Gln Leu Gly Pro Glu Ala Ala Ala Leu Arg Pro Gly Trp
1 5 10 15

Leu Ala Leu Leu Leu Trp Val Ser Ala Leu Ser Cys Ser Phe Ser Leu
20 25 30

Pro Ala Ser Ser Leu Ser Ser Leu Val Pro Gln Val Arg Thr Ser Tyr
35 40 45

Asn Phe Gly Arg Thr Phe Leu Gly Leu Asp Lys Cys Asn Ala Cys Ile
50 55 60

Gly Thr Ser Ile Cys Lys Lys Phe Phe Lys Glu Glu Ile Arg Ser Asp
65 70 75 80

Asn Trp Leu Ala Ser His Leu Gly Leu Pro Pro Asp Ser Leu Leu Ser
85 90 95

Tyr Pro Ala Asn Tyr Ser Asp Asp Ser Lys Ile Trp Arg Pro Val Glu
100 105 110

Ile Phe Arg Leu Val Ser Lys Tyr Gln Asn Glu Ile Ser Asp Arg Lys
115 120 125

Ile Cys Ala Ser Ala Ser Ala Pro Lys Thr Cys Ser Ile Glu Arg Val
130 135 140

Leu Arg Lys Thr Glu Arg Phe Gln Lys Trp Leu Gln Ala Lys Arg Leu
145 150 155 160

Thr Pro Asp Leu Val Gln Asp Cys His Gln Gly Gln Arg Glu Leu Lys
165 170 175

Phe Leu Cys Met Leu Arg
180

49321-142 SEQ LIST.txt

```

<210> 7
<211> 5668
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (163)..(2475)

<400> 7
gctttgtttg atggtgatcc acatttatcc acagagaatc ctgccttggt tcctgatgct      60

ttgctagcct cagacacttg tctggatata agcgaagctg cctttgacca cagtttcagc      120

gatgcctcag gtctcaacac atccacggga acaatagatg ac atg agt aaa ctg      174
                               Met Ser Lys Leu
                               1

aca tta tcc gaa ggc cat ccg gaa acg cca gtt gat ggg gac cta ggg      222
Thr Leu Ser Glu Gly His Pro Glu Thr Pro Val Asp Gly Asp Leu Gly
5                               10                               15                               20

aag caa gat atc tgc tca tct gaa gcc tcg tgg ggt gat ttt gaa tat      270
Lys Gln Asp Ile Cys Ser Ser Glu Ala Ser Trp Gly Asp Phe Glu Tyr
                               25                               30                               35

gat gta atg ggc cag aat atc gat gaa gat tta ctg aga gag cct gaa      318
Asp Val Met Gly Gln Asn Ile Asp Glu Asp Leu Leu Arg Glu Pro Glu
                               40                               45                               50

cac ttc ctg tat ggt ggt gac cct cct ttg gag gaa gat tct ctg aag      366
His Phe Leu Tyr Gly Gly Asp Pro Pro Leu Glu Glu Asp Ser Leu Lys
                               55                               60                               65

cag tcg ctg gca ccg tac aca cct ccc ttt gat ttg tct tat ctc aca      414
Gln Ser Leu Ala Pro Tyr Thr Pro Pro Phe Asp Leu Ser Tyr Leu Thr
                               70                               75                               80

gaa cct gcc cag agt gct gaa aca ata gag gaa gct ggg tct cca gag      462
Glu Pro Ala Gln Ser Ala Glu Thr Ile Glu Glu Ala Gly Ser Pro Glu
85                               90                               95                               100

gat gaa tct ctg gga tgc aga gca gca gag ata gtg ctt tct gca ctt      510
Asp Glu Ser Leu Gly Cys Arg Ala Ala Glu Ile Val Leu Ser Ala Leu
                               105                               110                               115

cct gat cga aga agt gag gga aac cag gct gag acc aaa aac aga ctg      558
Pro Asp Arg Arg Ser Glu Gly Asn Gln Ala Glu Thr Lys Asn Arg Leu
                               120                               125                               130

cct gga tcc cag ctg gct gtg ctg cat att cgt gaa gac cct gag tcc      606
Pro Gly Ser Gln Leu Ala Val Leu His Ile Arg Glu Asp Pro Glu Ser
                               135                               140                               145

gtt tat ttg ccg gta gga gca ggc tcc aac att ttg tct cca tca aac      654
Val Tyr Leu Pro Val Gly Ala Gly Ser Asn Ile Leu Ser Pro Ser Asn
                               150                               155                               160

```

49321-142 SEQ LIST.txt

gtt gac tgg gaa gta gaa aca gat aat tct gat tta cca gca ggt gga Val Asp Trp Glu Val Glu Thr Asp Asn Ser Asp Leu Pro Ala Gly Gly 165 170 175 180	702
gac ata gga cca cca aat ggt gcc agc aag gaa ata tca gaa ttg gaa Asp Ile Gly Pro Pro Asn Gly Ala Ser Lys Glu Ile Ser Glu Leu Glu 185 190 195	750
gaa gaa aaa aca att cct acc aaa gag cct gag cag ata aaa tca gaa Glu Glu Lys Thr Ile Pro Thr Lys Glu Pro Glu Gln Ile Lys Ser Glu 200 205 210	798
tac aag gaa gaa aga tgt aca gag aag aat gaa gat cgt cat gca cta Tyr Lys Glu Glu Arg Cys Thr Glu Lys Asn Glu Asp Arg His Ala Leu 215 220 225	846
cac atg gat tac ata ctt gta aac cgt gaa gaa aat tca cac tca aag His Met Asp Tyr Ile Leu Val Asn Arg Glu Glu Asn Ser His Ser Lys 230 235 240	894
cca gag acc tgt gaa gaa aga gaa agc ata gct gaa tta gaa ttg tat Pro Glu Thr Cys Glu Glu Arg Glu Ser Ile Ala Glu Leu Glu Leu Tyr 245 250 255 260	942
gta ggt tcc aaa gaa aca ggg ctg cag gga act cag tta gca agc ttc Val Gly Ser Lys Glu Thr Gly Leu Gln Gly Thr Gln Leu Ala Ser Phe 265 270 275	990
cca gac aca tgt cag cca gcc tcc tta aat gaa aga aaa ggt ctc tct Pro Asp Thr Cys Gln Pro Ala Ser Leu Asn Glu Arg Lys Gly Leu Ser 280 285 290	1038
gca gag aaa atg tct tct aaa agc gat acg aga tca tct ttt gaa agc Ala Glu Lys Met Ser Ser Lys Ser Asp Thr Arg Ser Ser Phe Glu Ser 295 300 305	1086
cct gca caa gac cag agt tgg atg ttc ttg ggc cat agt gag gtt ggt Pro Ala Gln Asp Gln Ser Trp Met Phe Leu Gly His Ser Glu Val Gly 310 315 320	1134
gat cca tca ctg gat gcc agg gac tca ggg cct ggg tgg tct ggc aag Asp Pro Ser Leu Asp Ala Arg Asp Ser Gly Pro Gly Trp Ser Gly Lys 325 330 335 340	1182
act gtg gag ccg ttc tct gaa ctc ggc ttg ggt gag ggt ccc cag ctg Thr Val Glu Pro Phe Ser Glu Leu Gly Leu Gly Glu Gly Pro Gln Leu 345 350 355	1230
cag att ctg gaa gaa atg aag cct cta gaa tct ttg gca cta gag gaa Gln Ile Leu Glu Glu Met Lys Pro Leu Glu Ser Leu Ala Leu Glu Glu 360 365 370	1278
gcc tct ggt cca gtc agc caa tca cag aag agt aag agc cga ggc agg Ala Ser Gly Pro Val Ser Gln Ser Gln Lys Ser Lys Ser Arg Gly Arg 375 380 385	1326
gct ggc ccg gat gca gtt acg ttg cag gct gtc acc cat gac aat gaa Ala Gly Pro Asp Ala Val Thr Leu Gln Ala Val Thr His Asp Asn Glu 390 395 400	1374

49321-142 SEQ LIST.txt

tgg gaa atg ctt tca cca cag cct gtt cag aaa aac atg atc cct gac	1422
Trp Glu Met Leu Ser Pro Gln Pro Val Gln Lys Asn Met Ile Pro Asp	
405 410 415 420	
acg gaa atg gag gag gag aca gag ttc ctt gag ctc gga acc agg ata	1470
Thr Glu Met Glu Glu Glu Thr Glu Phe Leu Glu Leu Gly Thr Arg Ile	
425 430 435	
tca aga cca aat gga cta ctg tca gag gat gta gga atg gac atc ccc	1518
Ser Arg Pro Asn Gly Leu Leu Ser Glu Asp Val Gly Met Asp Ile Pro	
440 445 450	
ttt gaa gag ggc gtg ctg agt ccc agt gct gca gac atg agg cct gaa	1566
Phe Glu Glu Gly Val Leu Ser Pro Ser Ala Ala Asp Met Arg Pro Glu	
455 460 465	
cct cct aat tct ctg gat ctt aat gac act cat cct cgg aga atc aag	1614
Pro Pro Asn Ser Leu Asp Leu Asn Asp Thr His Pro Arg Arg Ile Lys	
470 475 480	
ctc aca gcc cca aat atc aat ctt tct ctg gac caa agt gaa gga tct	1662
Leu Thr Ala Pro Asn Ile Asn Leu Ser Leu Asp Gln Ser Glu Gly Ser	
485 490 495 500	
att ctc tct gat gat aac ttg gac agt cca gat gaa att gac atc aat	1710
Ile Leu Ser Asp Asp Asn Leu Asp Ser Pro Asp Glu Ile Asp Ile Asn	
505 510 515	
gtg gat gaa ctt gat acc ccc gat gaa gca gat tct ttt gag tac act	1758
Val Asp Glu Leu Asp Thr Pro Asp Glu Ala Asp Ser Phe Glu Tyr Thr	
520 525 530	
ggc cat gat ccc aca gcc aac aaa gat tct ggc caa gag tca gag tct	1806
Gly His Asp Pro Thr Ala Asn Lys Asp Ser Gly Gln Glu Ser Glu Ser	
535 540 545	
att cca gaa tat acg gcc gaa gag gaa cgg gag gac aac cgg ctt tgg	1854
Ile Pro Glu Tyr Thr Ala Glu Glu Glu Arg Glu Asp Asn Arg Leu Trp	
550 555 560	
agg aca gtg gtc att gga gaa caa gag cag cgc att gac atg aag gtc	1902
Arg Thr Val Val Ile Gly Glu Gln Glu Gln Arg Ile Asp Met Lys Val	
565 570 575 580	
atc gag ccc tac agg aga gtc att tct cac gga gga tac tat ggg gac	1950
Ile Glu Pro Tyr Arg Arg Val Ile Ser His Gly Gly Tyr Tyr Gly Asp	
585 590 595	
ggc cta aat gcc atc att gtg ttt gcc gcc tgt ttt ctg cca gac agc	1998
Gly Leu Asn Ala Ile Ile Val Phe Ala Ala Cys Phe Leu Pro Asp Ser	
600 605 610	
agt cgg gcg gat tac cac tat gtc atg gaa aat ctt ttc cta tat gta	2046
Ser Arg Ala Asp Tyr His Tyr Val Met Glu Asn Leu Phe Leu Tyr Val	
615 620 625	
ata agt act tta gag ttg atg gta gct gaa gac tat atg att gtg tac	2094
Ile Ser Thr Leu Glu Leu Met Val Ala Glu Asp Tyr Met Ile Val Tyr	

49321-142 SEQ LIST.txt

630	635	640	
ttg aat ggt gca acc cca aga agg agg atg cca ggg cta ggc tgg atg			2142
Leu Asn Gly Ala Thr Pro Arg Arg Arg Met Pro Gly Leu Gly Trp Met			
645	650	655	660
aag aaa tgc tac cag atg att gac aga cgg ttg agg aag aat ttg aaa			2190
Lys Lys Cys Tyr Gln Met Ile Asp Arg Arg Leu Arg Lys Asn Leu Lys			
	665	670	675
tca ttc atc att gtt cat cca tct tgg ttc atc aga aca atc ctt gct			2238
Ser Phe Ile Ile Val His Pro Ser Trp Phe Ile Arg Thr Ile Leu Ala			
	680	685	690
gtg aca cga cct ttt ata agt tca aaa ttc agc agt aaa att aaa tat			2286
Val Thr Arg Pro Phe Ile Ser Ser Lys Phe Ser Ser Lys Ile Lys Tyr			
	695	700	705
gtc aat agc tta tca gaa ctc agt ggg ctg atc cca atg gat tgc atc			2334
Val Asn Ser Leu Ser Glu Leu Ser Gly Leu Ile Pro Met Asp Cys Ile			
	710	715	720
cac att cca gag agc atc atc aaa ctg gat gaa gaa ctg agg gaa gca			2382
His Ile Pro Glu Ser Ile Ile Lys Leu Asp Glu Glu Leu Arg Glu Ala			
	725	730	735
tca gag gca gct aaa act agc tgc ctt tac aat gat cca gaa atg tct			2430
Ser Glu Ala Ala Lys Thr Ser Cys Leu Tyr Asn Asp Pro Glu Met Ser			
	745	750	755
tct atg gag aag gat att gac ttg aag ctg aaa gaa aag cct tag			2475
Ser Met Glu Lys Asp Ile Asp Leu Lys Leu Lys Glu Lys Pro			
	760	765	770
ttggccatgc tggaagaaga ggatgctttt ctgggttcacg gttctgttga aacatatcta			2535
cctgaaagag acagggctga tgttaccttt ttccactttg cactacctgg tgccattcta			2595
aatttctaag gggaaaaata gaaagtttgt ttactcttaa gatattttat gaaattgtgt			2655
gtactttcct attttgccaa ttatgtgcct caaagatttt agttgagcct tagcaagaaa			2715
gtaggacctt ccatttcaat acttcattaa cacggtgtag tgatactttg tcccttagac			2775
tggtgtttac cagtaagata cctttaatcc actgttaagt atgagtggat ttgtttccat			2835
agattagctg gatttccttt tggtgattgc attaggttta aagtacacag gtctcaactc			2895
tccccaggaa agtttcccct gtttgactcc acctttaaaa tcctaagcct gactaggaca			2955
gccacaaacc acacaagggtg taaaaccatc atcagctaag tgcccgtttt gttcttgttt			3015
accagaatct cctttaactt ctcaaaggga agccgggctt tctaattccac gtcaacttta			3075
ttttagttgt caaattgggc attatatattt atgtaaattg gtcttttaac atcattttcc			3135
tgatgaatgt tggtgaccac cacattgtga aatttaagaa tccgtgttgc atgtttggta			3195
gctctctgag ttccaggcca taaactcagc tccagagggtt accttttaag tgccaagaac			3255

49321-142 SEQ LIST.txt

tcaagtgcaa ggtggcctac tcaaaaatca tttggttagca ttcagttatt catgaattcc	3315
tctctcgcac gcattataaa aagtgatctg ctttaaaaca ccgtaatctg atcataggct	3375
taaaattaaa tatgagtatt actttcatgt acaaaatatt tcctttatag tcttcatatg	3435
ccctttaaaa tgccaacaag atttcaagtc tgtaggcctc tagtgagggtg ggggtggcaaa	3495
ccacagctaa gtctcgctca ccactgcaag ctaagaatgg tttttacatt ttgggttgga	3555
aaaatttttt ttgaatattt catgacacat gaaaattatt caaatgttag tgccgataaa	3615
taaagtggta ctgaaacaca gccacacaaa cttgtttttg tactgtctac agctactttc	3675
acactacagc cgcagagctg agcagttcag cagaccgtat gtcccacaat gcctaaaaca	3735
ttgactatgt ttacagaaaa agtttgctga ccctgctct agcaaacgca tcctttccta	3795
ctccacccca atttgtattt agatagtttc tctaacagaa cggacaaatg aggctgcaaa	3855
ctaattttatt tttgtcaaaa atcaatgttt tgacatccac agacagtga ataaaagaaa	3915
tggtctgctg aaaaacatga ggagtcctag ccacaaaatc actgcttagg ttgcaattgc	3975
caaaatgaag ctttcttaga agcacttctt tagtatatac aggtgttggc tgaagtcctg	4035
gcctcactct gggaaccatt cttagtctcc agtgtctcct attacaaaga agctggcaga	4095
aataaaaaatg aaggggtgag agcgggtcca ccctagtctc atgggtggaaa attcattggg	4155
gagagctgtc caggatattt ggagtcctgg gtagaaggag cttgtaacta ctttaaagtc	4215
gacatctttg cacagggtgat tgagtttctc tgacctcatt gcttcacctc tgtctcctcc	4275
cgtccttccg cacgtgcca cacacacgca gttcagccct ctttcctcca taagcctcca	4335
tcgttttctc ttttctcctc ttgatccttt caagcgagta tcttggtgaa ttgtatgttc	4395
tggttgatct cctccttcat aacatctggc ttgttgga gaaaaaccct acagcccacc	4455
ccctcccaca gccacctcc acttttgaaa gcccaaatta cacctctccc agaacacagt	4515
gttgacgtaa atacagttac ccaatattcc tgtttgttca cctatttgct actttcactc	4575
agtagcatcc cattttgtaa aatgaattcc atgggtcacc tgtcacagga agtaatgaaa	4635
aatccagtgt tcagtgtagt ggtgcaaacc tgagggcata gagctgttca tagagggctc	4695
ttgttatagc caaacagaca cagcaacaat ctcaccattt atatatatat ttttaacttg	4755
tccagctcat ctatggaaaa ctactcaggt ggtatgctgt ttgaagcctc atcttcctac	4815
atgaaaatta tgggcatttg tccaatgat tttgtttcag ctgttctgta ggctgcataa	4875
ccactctgat atttaggtat ctgctatttt attatcttaa aagacaaatt aatttaattg	4935
catgtgctag ggaaaagcta ccatgtacat tcacccaag taaatagaat cctagatgaa	4995

49321-142 SEQ LIST.txt

tcctagaaaa ataatcccta agcagatagg tagacagagg taaacattca catgatttag 5055
ctctctagct cttgcactct gaacattctt gctttggttc tgacttctgg gaactgcttt 5115
gcatttctcc tatagatctg tagttaaggg aaccaagggg tcattggggc aaaagcattg 5175
tttctcaaag ctcccttgatt aagagaaaga acagaaattt gcacagaaga tagtgtcaag 5235
gagtgagaaa gtttgtttga gggcagtagc tcagtgtgga agaaaatcct gaagtttctg 5295
ttgaagccat acaatgttct atgggggttac tctctaagac attctctgag gtgtgtgagg 5355
aagtcactac tcctagcctt tgттаagatg taattttaaa tattcagtta tggtagctatg 5415
tttgcaactc tcgtcttatt acaatgcctc agtagtttgt tcccttagaa acatttagat 5475
gtgcacaaat taatctttta tatatctaaa ggtttttcta tcatgcattg gattgctcag 5535
aataaagtgt ctgtagact tcgttttggt aaataaattc tccataatgt agattaataa 5595
tataaaagtc tttaatgaca caatatatct atatagcctc actgtataat tcagaaataa 5655
aaattgattc tgc 5668

<210> 8
<211> 770
<212> PRT
<213> homo sapiens
<400> 8

Met Ser Lys Leu Thr Leu Ser Glu Gly His Pro Glu Thr Pro Val Asp
1 5 10 15

Gly Asp Leu Gly Lys Gln Asp Ile Cys Ser Ser Glu Ala Ser Trp Gly
20 25 30

Asp Phe Glu Tyr Asp Val Met Gly Gln Asn Ile Asp Glu Asp Leu Leu
35 40 45

Arg Glu Pro Glu His Phe Leu Tyr Gly Gly Asp Pro Pro Leu Glu Glu
50 55 60

Asp Ser Leu Lys Gln Ser Leu Ala Pro Tyr Thr Pro Pro Phe Asp Leu
65 70 75 80

Ser Tyr Leu Thr Glu Pro Ala Gln Ser Ala Glu Thr Ile Glu Glu Ala
85 90 95

Gly Ser Pro Glu Asp Glu Ser Leu Gly Cys Arg Ala Ala Glu Ile Val
100 105 110

49321-142 SEQ LIST.txt

Leu Ser Ala Leu Pro Asp Arg Arg Ser Glu Gly Asn Gln Ala Glu Thr
115 120 125

Lys Asn Arg Leu Pro Gly Ser Gln Leu Ala Val Leu His Ile Arg Glu
130 135 140

Asp Pro Glu Ser Val Tyr Leu Pro Val Gly Ala Gly Ser Asn Ile Leu
145 150 155 160

Ser Pro Ser Asn Val Asp Trp Glu Val Glu Thr Asp Asn Ser Asp Leu
165 170 175

Pro Ala Gly Gly Asp Ile Gly Pro Pro Asn Gly Ala Ser Lys Glu Ile
180 185 190

Ser Glu Leu Glu Glu Glu Lys Thr Ile Pro Thr Lys Glu Pro Glu Gln
195 200 205

Ile Lys Ser Glu Tyr Lys Glu Glu Arg Cys Thr Glu Lys Asn Glu Asp
210 215 220

Arg His Ala Leu His Met Asp Tyr Ile Leu Val Asn Arg Glu Glu Asn
225 230 235 240

Ser His Ser Lys Pro Glu Thr Cys Glu Glu Arg Glu Ser Ile Ala Glu
245 250 255

Leu Glu Leu Tyr Val Gly Ser Lys Glu Thr Gly Leu Gln Gly Thr Gln
260 265 270

Leu Ala Ser Phe Pro Asp Thr Cys Gln Pro Ala Ser Leu Asn Glu Arg
275 280 285

Lys Gly Leu Ser Ala Glu Lys Met Ser Ser Lys Ser Asp Thr Arg Ser
290 295 300

Ser Phe Glu Ser Pro Ala Gln Asp Gln Ser Trp Met Phe Leu Gly His
305 310 315 320

Ser Glu Val Gly Asp Pro Ser Leu Asp Ala Arg Asp Ser Gly Pro Gly
325 330 335

Trp Ser Gly Lys Thr Val Glu Pro Phe Ser Glu Leu Gly Leu Gly Glu
340 345 350

49321-142 SEQ LIST.txt

Gly Pro Gln Leu Gln Ile Leu Glu Glu Met Lys Pro Leu Glu Ser Leu
355 360 365

Ala Leu Glu Glu Ala Ser Gly Pro Val Ser Gln Ser Gln Lys Ser Lys
370 375 380

Ser Arg Gly Arg Ala Gly Pro Asp Ala Val Thr Leu Gln Ala Val Thr
385 390 395 400

His Asp Asn Glu Trp Glu Met Leu Ser Pro Gln Pro Val Gln Lys Asn
405 410 415

Met Ile Pro Asp Thr Glu Met Glu Glu Glu Thr Glu Phe Leu Glu Leu
420 425 430

Gly Thr Arg Ile Ser Arg Pro Asn Gly Leu Leu Ser Glu Asp Val Gly
435 440 445

Met Asp Ile Pro Phe Glu Glu Gly Val Leu Ser Pro Ser Ala Ala Asp
450 455 460

Met Arg Pro Glu Pro Pro Asn Ser Leu Asp Leu Asn Asp Thr His Pro
465 470 475 480

Arg Arg Ile Lys Leu Thr Ala Pro Asn Ile Asn Leu Ser Leu Asp Gln
485 490 495

Ser Glu Gly Ser Ile Leu Ser Asp Asp Asn Leu Asp Ser Pro Asp Glu
500 505 510

Ile Asp Ile Asn Val Asp Glu Leu Asp Thr Pro Asp Glu Ala Asp Ser
515 520 525

Phe Glu Tyr Thr Gly His Asp Pro Thr Ala Asn Lys Asp Ser Gly Gln
530 535 540

Glu Ser Glu Ser Ile Pro Glu Tyr Thr Ala Glu Glu Glu Arg Glu Asp
545 550 555 560

Asn Arg Leu Trp Arg Thr Val Val Ile Gly Glu Gln Glu Gln Arg Ile
565 570 575

Asp Met Lys Val Ile Glu Pro Tyr Arg Arg Val Ile Ser His Gly Gly

49321-142 SEQ LIST.txt
585 590

580

Tyr Tyr Gly Asp Gly Leu Asn Ala Ile Ile Val Phe Ala Ala Cys Phe
595 600 605

Leu Pro Asp Ser Ser Arg Ala Asp Tyr His Tyr Val Met Glu Asn Leu
610 615 620

Phe Leu Tyr Val Ile Ser Thr Leu Glu Leu Met Val Ala Glu Asp Tyr
625 630 635 640

Met Ile Val Tyr Leu Asn Gly Ala Thr Pro Arg Arg Arg Met Pro Gly
645 650 655

Leu Gly Trp Met Lys Lys Cys Tyr Gln Met Ile Asp Arg Arg Leu Arg
660 665 670

Lys Asn Leu Lys Ser Phe Ile Ile Val His Pro Ser Trp Phe Ile Arg
675 680 685

Thr Ile Leu Ala Val Thr Arg Pro Phe Ile Ser Ser Lys Phe Ser Ser
690 695 700

Lys Ile Lys Tyr Val Asn Ser Leu Ser Glu Leu Ser Gly Leu Ile Pro
705 710 715 720

Met Asp Cys Ile His Ile Pro Glu Ser Ile Ile Lys Leu Asp Glu Glu
725 730 735

Leu Arg Glu Ala Ser Glu Ala Ala Lys Thr Ser Cys Leu Tyr Asn Asp
740 745 750

Pro Glu Met Ser Ser Met Glu Lys Asp Ile Asp Leu Lys Leu Lys Glu
755 760 765

Lys Pro
770

<210> 9
<211> 1589
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

49321-142 SEQ LIST.txt

<222> (169)..(597)

<400> 9

```

gtctcttctct cgtctcctct ctttctctcc tccctctgcc ttcccagtgc ataaagtctc      60
tgctgctccc ggaacttggt ggcaatgcct attttttggc tttccccgcg gttctctaaa      120
ctaactatatt aaaggtctgc ggtcgcaaat ggtttgacta aacgtagg atg gga ctt      177
                                   Met Gly Leu
                                   1

aag ttg aac ggc aga tat att tca ctg atc ctc gcg gtg caa ata gcg      225
Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val Gln Ile Ala
   5                                10                                15

tat ctg gtg cag gcc gtg aga gca gcg ggc aag tgc gat gcg gtc ttc      273
Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp Ala Val Phe
  20                                25                                30                                35

aag ggc ttt tcg gac tgt ttg ctc aag ctg ggc gac agc atg gcc aac      321
Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser Met Ala Asn
                   40                                45                                50

tac ccg cag ggc ctg gac gac aag acg aac atc aag acc gtg tgc aca      369
Tyr Pro Gln Gly Leu Asp Asp Lys Thr Asn Ile Lys Thr Val Cys Thr
                   55                                60                                65

tac tgg gag gat ttc cac agc tgc acg gtc aca gcc ctt acg gat tgc      417
Tyr Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala Leu Thr Asp Cys
                   70                                75                                80

cag gaa ggg gcg aaa gat atg tgg gat aaa ctg aga aaa gaa tcc aaa      465
Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys Glu Ser Lys
   85                                90                                95

aac ctc aac atc caa ggc agc tta ttc gaa ctc tgc ggc agc ggc aac      513
Asn Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys Gly Ser Gly Asn
 100                                105                                110                                115

ggg gcg gcg ggg tcc ctg ctc ccg gcg ttc ccg gtg ctc ctg gtg tct      561
Gly Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val Leu Leu Val Ser
                   120                                125                                130

ctc tcg gca gct tta gcg acc tgg ctt tcc ttc tga gcgtggggcc      607
Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe
                   135                                140

agctcccccc gcgcgcccac ccacactcac tccatgctcc cggaaatcga gaggaagatc      667
cattagttct ttggggacgt tgtgattctc tgtgatgctg aaaacactca tataggattg      727
tgggaaatcc tgattctctt ttttatttcg tttgatttct tgtgttttat ttgccaaatg      787
ttaccaatca gtgagcaagc aagcacagcc aaaatcggac ctcagcttta gtccgtcttc      847
acacacaaat aagaaaacgg caaaccacc ccatttttta attttattat tattaatttt      907
ttttgttggc aaaagaatct caggaacggc cctggggccac ctactatatt aatcatgcta      967

```

49321-142 SEQ LIST.txt

gtaacatgaa aaatgatggg ctctctcctaa taggaaggcg aggagaggag aaggccaggg 1027
 gaatgaattc aagagagatg tccacggccg aacatacgg tgaataattc acgctcacgt 1087
 cgttcttcca cagtatcttg ttttgatcat ttccactgca ctttctcct caagaaaagc 1147
 gaaaggacag actgttggct ttgtgtttgg aggataggag ggagagaggg aaggggctga 1207
 ggaaatctct ggggtaagag taaaggcttc cagaagacat gctgctatgg tctactgaggg 1267
 gttagcttta tctgctgttg ttgatgcac cgtccaagtt cactgccttt attttcctc 1327
 ctccctcttg ttttagctgt tacacacaca gtaatacctg aatatccaac ggtatagatc 1387
 acaagggggg gatgttaaatt gttaatctaa aatatagcta aaaaaagatt ttgacataaa 1447
 agagccttga ttttaaaaaa aaaagagaga gagatgtaat ttaaaaagtt tattataaat 1507
 taaattcagc aaaaaaagat ttgctacaaa gtatagagaa gtataaaata aaagttattg 1567
 tttgaaaaaa aaaaaaaaaa aa 1589

<210> 10
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val
 1 5 10 15

Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp
 20 25 30

Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser
 35 40 45

Met Ala Asn Tyr Pro Gln Gly Leu Asp Asp Lys Thr Asn Ile Lys Thr
 50 55 60

Val Cys Thr Tyr Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala Leu
 65 70 75 80

Thr Asp Cys Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys
 85 90 95

Glu Ser Lys Asn Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys Gly
 100 105 110

Ser Gly Asn Gly Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val Leu

49321-142 SEQ LIST.txt

115

120

125

Leu Val Ser Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe
 130 135 140

<210> 11
 <211> 5180
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)..(4161)

<400> 11
 accgggagcg cgcgctctga tccgaggaga ccccgcgctc ccgcagcc atg ggc acc 57
 Met Gly Thr
 1

ggg ggc cgg cgg ggg gcg gcg gcc gcg ccg ctg ctg gtg gcg gtg gcc 105
 Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val Ala Val Ala
 5 10 15

gcg ctg cta ctg ggc gcc gcg ggc cac ctg tac ccc gga gag gtg tgt 153
 Ala Leu Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly Glu Val Cys
 20 25 30 35

ccc ggc atg gat atc cgg aac aac ctc act agg ttg cat gag ctg gag 201
 Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His Glu Leu Glu
 40 45 50

aat tgc tct gtc atc gaa gga cac ttg cag ata ctc ttg atg ttc aaa 249
 Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu Met Phe Lys
 55 60 65

acg agg ccc gaa gat ttc cga gac ctc agt ttc ccc aaa ctc atc atg 297
 Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys Leu Ile Met
 70 75 80

atc act gat tac ttg ctg ctc ttc cgg gtc tat ggg ctc gag agc ctg 345
 Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu Glu Ser Leu
 85 90 95

aag gac ctg ttc ccc aac ctc acg gtc atc cgg gga tca cga ctg ttc 393
 Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser Arg Leu Phe
 100 105 110 115

ttt aac tac gcg ctg gtc atc ttc gag atg gtt cac ctc aag gaa ctc 441
 Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu Lys Glu Leu
 120 125 130

ggc ctc tac aac ctg atg aac atc acc cgg ggt tct gtc cgc atc gag 489
 Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val Arg Ile Glu
 135 140 145

aag aac aat gag ctc tgt tac ttg gcc act atc gac tgg tcc cgt atc 537

49321-142 SEQ LIST.txt

Lys	Asn	Asn	Glu	Leu	Cys	Tyr	Leu	Ala	Thr	Ile	Asp	Trp	Ser	Arg	Ile		
	150						155					160					
ctg	gat	tcc	gtg	gag	gat	aat	tac	atc	gtg	ttg	aac	aaa	gat	gac	aac	585	
Leu	Asp	Ser	Val	Glu	Asp	Asn	Tyr	Ile	Val	Leu	Asn	Lys	Asp	Asp	Asn		
	165					170					175						
gag	gag	tgt	gga	gac	atc	tgt	ccg	ggc	acc	gcg	aag	ggc	aag	acc	aac	633	
Glu	Glu	Cys	Gly	Asp	Ile	Cys	Pro	Gly	Thr	Ala	Lys	Gly	Lys	Thr	Asn		
180					185					190					195		
tgc	ccc	gcc	acc	gtc	atc	aac	ggg	cag	ttt	gtc	gaa	cga	tgt	tgg	act	681	
Cys	Pro	Ala	Thr	Val	Ile	Asn	Gly	Gln	Phe	Val	Glu	Arg	Cys	Trp	Thr		
				200					205					210			
cat	agt	cac	tgc	cag	aaa	gtt	tgc	ccg	acc	atc	tgt	aag	tca	cac	ggc	729	
His	Ser	His	Cys	Gln	Lys	Val	Cys	Pro	Thr	Ile	Cys	Lys	Ser	His	Gly		
			215					220					225				
tgc	acc	gcc	gaa	ggc	ctc	tgt	tgc	cac	agc	gag	tgc	ctg	ggc	aac	tgt	777	
Cys	Thr	Ala	Glu	Gly	Leu	Cys	Cys	His	Ser	Glu	Cys	Leu	Gly	Asn	Cys		
	230					235						240					
tct	cag	ccc	gac	gac	ccc	acc	aag	tgc	gtg	gcc	tgc	cgc	aac	ttc	tac	825	
Ser	Gln	Pro	Asp	Asp	Pro	Thr	Lys	Cys	Val	Ala	Cys	Arg	Asn	Phe	Tyr		
	245					250					255						
ctg	gac	ggc	agg	tgt	gtg	gag	acc	tgc	ccg	ccc	ccg	tac	tac	cac	ttc	873	
Leu	Asp	Gly	Arg	Cys	Val	Glu	Thr	Cys	Pro	Pro	Pro	Tyr	Tyr	His	Phe		
260					265				270						275		
cag	gac	tgg	cgc	tgt	gtg	aac	ttc	agc	ttc	tgc	cag	gac	ctg	cac	cac	921	
Gln	Asp	Trp	Arg	Cys	Val	Asn	Phe	Ser	Phe	Cys	Gln	Asp	Leu	His	His		
				280					285					290			
aaa	tgc	aag	aac	tcg	cgg	agg	cag	ggc	tgc	cac	cag	tac	gtc	att	cac	969	
Lys	Cys	Lys	Asn	Ser	Arg	Arg	Gln	Gly	Cys	His	Gln	Tyr	Val	Ile	His		
			295					300					305				
aac	aac	aag	tgc	atc	cct	gag	tgt	ccc	tcc	ggg	tac	acg	atg	aat	tcc	1017	
Asn	Asn	Lys	Cys	Ile	Pro	Glu	Cys	Pro	Ser	Gly	Tyr	Thr	Met	Asn	Ser		
		310					315						320				
agc	aac	ttg	ctg	tgc	acc	cca	tgc	ctg	ggc	ccc	tgt	ccc	aag	gtg	tgc	1065	
Ser	Asn	Leu	Leu	Cys	Thr	Pro	Cys	Leu	Gly	Pro	Cys	Pro	Lys	Val	Cys		
	325					330					335						
cac	ctc	cta	gaa	ggc	gag	aag	acc	atc	gac	tcg	gtg	acg	tct	gcc	cag	1113	
His	Leu	Leu	Glu	Gly	Glu	Lys	Thr	Ile	Asp	Ser	Val	Thr	Ser	Ala	Gln		
340					345					350					355		
gag	ctc	cga	gga	tgc	acc	gtc	atc	aac	ggg	agt	ctg	atc	atc	aac	att	1161	
Glu	Leu	Arg	Gly	Cys	Thr	Val	Ile	Asn	Gly	Ser	Leu	Ile	Ile	Asn	Ile		
				360					365					370			
cga	gga	ggc	aac	aat	ctg	gca	gct	gag	cta	gaa	gcc	aac	ctc	ggc	ctc	1209	
Arg	Gly	Gly	Asn	Asn	Leu	Ala	Ala	Glu	Leu	Glu	Ala	Asn	Leu	Gly	Leu		
			375					380					385				

49321-142 SEQ LIST.txt

att gaa gaa att tca ggg tat cta aaa atc cgc cga tcc tac gct ctg Ile Glu Glu Ile Ser Gly Tyr Leu Lys Ile Arg Arg Ser Tyr Ala Leu 390 395 400	1257
gtg tca ctt tcc ttc ttc cgg aag tta cgt ctg att cga gga gag acc Val Ser Leu Ser Phe Phe Arg Lys Leu Arg Leu Ile Arg Gly Glu Thr 405 410 415	1305
ttg gaa att ggg aac tac tcc ttc tat gcc ttg gac aac cag aac cta Leu Glu Ile Gly Asn Tyr Ser Phe Tyr Ala Leu Asp Asn Gln Asn Leu 420 425 430 435	1353
agg cag ctc tgg gac tgg agc aaa cac aac ctc acc atc act cag ggg Arg Gln Leu Trp Asp Trp Ser Lys His Asn Leu Thr Ile Thr Gln Gly 440 445 450	1401
aaa ctc ttc ttc cac tat aac ccc aaa ctc tgc ttg tca gaa atc cac Lys Leu Phe Phe His Tyr Asn Pro Lys Leu Cys Leu Ser Glu Ile His 455 460 465	1449
aag atg gaa gaa gtt tca gga acc aag ggg cgc cag gag aga aac gac Lys Met Glu Glu Val Ser Gly Thr Lys Gly Arg Gln Glu Arg Asn Asp 470 475 480	1497
att gcc ctg aag acc aat ggg gac cag gca tcc tgt gaa aat gag tta Ile Ala Leu Lys Thr Asn Gly Asp Gln Ala Ser Cys Glu Asn Glu Leu 485 490 495	1545
ctt aaa ttt tct tac att cgg aca tct ttt gac aag atc ttg ctg aga Leu Lys Phe Ser Tyr Ile Arg Thr Ser Phe Asp Lys Ile Leu Leu Arg 500 505 510 515	1593
tgg gag ccg tac tgg ccc ccc gac ttc cga gac ctc ttg ggg ttc atg Trp Glu Pro Tyr Trp Pro Pro Asp Phe Arg Asp Leu Leu Gly Phe Met 520 525 530	1641
ctg ttc tac aaa gag gcc cct tat cag aat gtg acg gag ttc gac ggg Leu Phe Tyr Lys Glu Ala Pro Tyr Gln Asn Val Thr Glu Phe Asp Gly 535 540 545	1689
cag gat gca tgt ggt tcc aac agt tgg acg gtg gta gac att gac cca Gln Asp Ala Cys Gly Ser Asn Ser Trp Thr Val Val Asp Ile Asp Pro 550 555 560	1737
ccc ctg agg tcc aac gac ccc aaa tca cag aac cac cca ggg tgg ctg Pro Leu Arg Ser Asn Asp Pro Lys Ser Gln Asn His Pro Gly Trp Leu 565 570 575	1785
atg cgg ggt ctc aag ccc tgg acc cag tat gcc atc ttt gtg aag acc Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe Val Lys Thr 580 585 590 595	1833
ctg gtc acc ttt tcg gat gaa cgc cgg acc tat ggg gcc aag agt gac Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala Lys Ser Asp 600 605 610	1881
atc att tat gtc cag aca gat gcc acc aac ccc tct gtg ccc ctg gat Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val Pro Leu Asp 615 620 625	1929

49321-142 SEQ LIST.txt

cca atc tca gtg tct aac tca tca tcc cag att att ctg aag tgg aaa	1977
Pro Ile Ser Val Ser Asn Ser Ser Ser Gln Ile Ile Leu Lys Trp Lys	
630 635 640	
cca ccc tcc gac ccc aat ggc aac atc acc cac tac ctg gtt ttc tgg	2025
Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu Val Phe Trp	
645 650 655	
gag agg cag gcg gaa gac agt gag ctg ttc gag ctg gat tat tgc ctc	2073
Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp Tyr Cys Leu	
660 665 670 675	
aaa ggg ctg aag ctg ccc tcg agg acc tgg tct cca cca ttc gag tct	2121
Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro Phe Glu Ser	
680 685 690	
gaa gat tct cag aag cac aac cag agt gag tat gag gat tcg gcc ggc	2169
Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp Ser Ala Gly	
695 700 705	
gaa tgc tgc tcc tgt cca aag aca gac tct cag atc ctg aag gag ctg	2217
Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu Lys Glu Leu	
710 715 720	
gag gag tcc tcg ttt agg aag acg ttt gag gat tac ctg cac aac gtg	2265
Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu His Asn Val	
725 730 735	
gtt ttc gtc ccc agg cca tct cgg aaa cgc agg tcc ctt ggc gat gtt	2313
Val Phe Val Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val	
740 745 750 755	
ggg aat gtg acg gtg gcc gtg ccc acg gtg gca gct ttc ccc aac act	2361
Gly Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr	
760 765 770	
tcc tcg acc agc gtg ccc acg agt ccg gag gag cac agg cct ttt gag	2409
Ser Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu	
775 780 785	
aag gtg gtg aac aag gag tcg ctg gtc atc tcc ggc ttg cga cac ttc	2457
Lys Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe	
790 795 800	
acg ggc tat cgc atc gag ctg cag gct tgc aac cag gac acc cct gag	2505
Thr Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu	
805 810 815	
gaa cgg tgc agt gtg gca gcc tac gtc agt gcg agg acc atg cct gaa	2553
Glu Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu	
820 825 830 835	
gcc aag gct gat gac att gtt ggc cct gtg acg cat gaa atc ttt gag	2601
Ala Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu	
840 845 850	
aac aac gtc gtc cac ttg atg tgg cag gag ccg aag gag ccc aat ggt	2649
Asn Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly	

49321-142 SEQ LIST.txt

855	860	865	
ctg atc gtg ctg tat gaa gtg agt tat cgg cga tat ggt gat gag gag Leu Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu 870 875 880			2697
ctg cat ctc tgc gtc tcc cgc aag cac ttc gct ctg gaa cgg ggc tgc Leu His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys 885 890 895			2745
agg ctg cgt ggg ctg tca ccg ggg aac tac agc gtg cga atc cgg gcc Arg Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala 900 905 910 915			2793
acc tcc ctt gcg ggc aac ggc tct tgg acg gaa ccc acc tat ttc tac Thr Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr 920 925 930			2841
gtg aca gac tat tta gac gtc ccg tca aat att gca aaa att atc atc Val Thr Asp Tyr Leu Asp Val Pro Ser Asn Ile Ala Lys Ile Ile Ile 935 940 945			2889
ggc ccc ctc atc ttt gtc ttt ctc ttc agt gtt gtg att gga agt att Gly Pro Leu Ile Phe Val Phe Leu Phe Ser Val Val Ile Gly Ser Ile 950 955 960			2937
tat cta ttc ctg aga aag agg cag cca gat ggg ccg ctg gga ccg ctt Tyr Leu Phe Leu Arg Lys Arg Gln Pro Asp Gly Pro Leu Gly Pro Leu 965 970 975			2985
tac gct tct tca aac cct gag tat ctc agt gcc agt gat gtg ttt cca Tyr Ala Ser Ser Asn Pro Glu Tyr Leu Ser Ala Ser Asp Val Phe Pro 980 985 990 995			3033
tgc tct gtg tac gtg ccg gac gag tgg gag gtg tct cga gag aag Cys Ser Val Tyr Val Pro Asp Glu Trp Glu Val Ser Arg Glu Lys 1000 1005 1010			3078
atc acc ctc ctt cga gag ctg ggg cag ggc tcc ttc ggc atg gtg Ile Thr Leu Leu Arg Glu Leu Gly Gln Gly Ser Phe Gly Met Val 1015 1020 1025			3123
tat gag ggc aat gcc agg gac atc atc aag ggt gag gca gag acc Tyr Glu Gly Asn Ala Arg Asp Ile Ile Lys Gly Glu Ala Glu Thr 1030 1035 1040			3168
cgc gtg gcg gtg aag acg gtc aac gag tca gcc agt ctc cga gag Arg Val Ala Val Lys Thr Val Asn Glu Ser Ala Ser Leu Arg Glu 1045 1050 1055			3213
cgg att gag ttc ctc aat gag gcc tcg gtc atg aag ggc ttc acc Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Gly Phe Thr 1060 1065 1070			3258
tgc cat cac gtg gtg cgc ctc ctg gga gtg gtg tcc aag ggc cag Cys His His Val Val Arg Leu Leu Gly Val Val Ser Lys Gly Gln 1075 1080 1085			3303
ccc acg ctg gtg gtg atg gag ctg atg gct cac gga gac ctg aag			3348

49321-142 SEQ LIST.txt

Pro Thr Leu Val Val Met Glu Leu Met Ala His Gly Asp Leu Lys	
1090 1095 1100	
agc tac ctc cgt tct ctg cgg cca gag gct gag aat aat cct ggc	3393
Ser Tyr Leu Arg Ser Leu Arg Pro Glu Ala Glu Asn Asn Pro Gly	
1105 1110 1115	
cgc cct ccc cct acc ctt caa gag atg att cag atg gcg gca gag	3438
Arg Pro Pro Pro Thr Leu Gln Glu Met Ile Gln Met Ala Ala Glu	
1120 1125 1130	
att gct gac ggg atg gcc tac ctg aac gcc aag aag ttt gtg cat	3483
Ile Ala Asp Gly Met Ala Tyr Leu Asn Ala Lys Lys Phe Val His	
1135 1140 1145	
cgg gac ctg gca gcg aga aac tgc atg gtc gcc cat gat ttt act	3528
Arg Asp Leu Ala Ala Arg Asn Cys Met Val Ala His Asp Phe Thr	
1150 1155 1160	
gtc aaa att gga gac ttt gga atg acc aga gac atc tat gaa acg	3573
Val Lys Ile Gly Asp Phe Gly Met Thr Arg Asp Ile Tyr Glu Thr	
1165 1170 1175	
gat tac tac cgg aaa ggg ggc aag ggt ctg ctc cct gta cgg tgg	3618
Asp Tyr Tyr Arg Lys Gly Gly Lys Gly Leu Leu Pro Val Arg Trp	
1180 1185 1190	
atg gca ccg gag tcc ctg aag gat ggg gtc ttc acc act tct tct	3663
Met Ala Pro Glu Ser Leu Lys Asp Gly Val Phe Thr Thr Ser Ser	
1195 1200 1205	
gac atg tgg tcc ttt ggc gtg gtc ctt tgg gaa atc acc agc ttg	3708
Asp Met Trp Ser Phe Gly Val Val Leu Trp Glu Ile Thr Ser Leu	
1210 1215 1220	
gca gaa cag cct tac caa ggc ctg tct aat gaa cag gtg ttg aaa	3753
Ala Glu Gln Pro Tyr Gln Gly Leu Ser Asn Glu Gln Val Leu Lys	
1225 1230 1235	
ttt gtc atg gat gga ggg tat ctg gat caa ccc gac aac tgt cca	3798
Phe Val Met Asp Gly Gly Tyr Leu Asp Gln Pro Asp Asn Cys Pro	
1240 1245 1250	
gag aga gtc act gac ctc atg cgc atg tgc tgg caa ttc aac ccc	3843
Glu Arg Val Thr Asp Leu Met Arg Met Cys Trp Gln Phe Asn Pro	
1255 1260 1265	
aac atg agg cca acc ttc ctg gag att gtc aac ctg ctc aag gac	3888
Asn Met Arg Pro Thr Phe Leu Glu Ile Val Asn Leu Leu Lys Asp	
1270 1275 1280	
gac ctg cac ccc agc ttt cca gag gtg tgc ttc ttc cac agc gag	3933
Asp Leu His Pro Ser Phe Pro Glu Val Ser Phe Phe His Ser Glu	
1285 1290 1295	
gag aac aag gct ccc gag agt gag gag ctg gag atg gag ttt gag	3978
Glu Asn Lys Ala Pro Glu Ser Glu Glu Leu Glu Met Glu Phe Glu	
1300 1305 1310	

49321-142 SEQ LIST.txt

gac atg gag aat gtg ccc ctg gac cgt tcc tcg cac tgt cag agg	4023
Asp Met Glu Asn Val Pro Leu Asp Arg Ser Ser His Cys Gln Arg	
1315 1320 1325	
gag gag gcg ggg ggc cgg gat gga ggg tcc tcg ctg ggt ttc aag	4068
Glu Glu Ala Gly Gly Arg Asp Gly Gly Ser Ser Leu Gly Phe Lys	
1330 1335 1340	
cgg agc tac gag gaa cac atc cct tac aca cac atg aac gga ggc	4113
Arg Ser Tyr Glu Glu His Ile Pro Tyr Thr His Met Asn Gly Gly	
1345 1350 1355	
aag aaa aac ggg cgg att ctg acc ttg cct cgg tcc aat cct tcc	4158
Lys Lys Asn Gly Arg Ile Leu Thr Leu Pro Arg Ser Asn Pro Ser	
1360 1365 1370	
taa cagtgcctac cgtggcgggg gcgggcaggg gttcccatTT tcgctttcct	4211
ctggtttgaa agcctctgga aaactcagga ttctcacgac tctaccatgt ccaatggagt	4271
tcagagatcg ttcctataca tttctgttca tcttaagggtg gactcgtttg gttaccaatt	4331
taactagtcc tgcagaggat ttaactgtga acctggaggg caaggggttt ccacagttgc	4391
tgctcctttg gggcaacgac ggtttcaaac caggattttg tgttttttcg ttccccccac	4451
ccgccccag cagatggaaa gaaagcacct gttttttacaa attctttttt tttttttttt	4511
tttttgctgg tgtctgagct tcagtataaa agacaaaact tcctgtttgt ggaacaaaag	4571
ttcgaaagaa aaaacaaaac aaaaacaccc agccctgttc caggagaatt tcaagtttta	4631
caggttgagc ttcaagatgg tttttttggg tttttttttt tctctcatcc aggctgaagg	4691
atTTTTTTTT tcttttcaaaa atgagttcct caaattgacc aatagctgct gctttcatat	4751
tttgataag ggtctgtggg cccggcgtgt gctcacgtgt gtatgcacgt gtgtgtgtcc	4811
attagacacg gctgacgtgt gtgcaaagta tccatgcgga gttgatgctt tgggaattgg	4871
ctcatgaagg ttcttctcaa gggTgcgagc tcatccccct ctctccttcc ttcttattga	4931
ctgggagact gtgctctcga cagattcttc ttgtgtcaga agtctagcct caggttttcta	4991
ccctcccttc acattgggtg ccaagggagg agcatttcat ttggagtgat tatgaatctt	5051
ttcaagacca aaccaagcta ggacattaaa aaaaaaaaaa agaaaaagaa agaaaaaaca	5111
aaatggaaaa aggaaaaaaa aaaagaactg agatgacaga gttttgagaa tatatttgta	5171
ccatatttta	5180
<210> 12	
<211> 1370	
<212> PRT	
<213> Homo sapiens	
<400> 12	

49321-142 SEQ LIST.txt

```

Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
1          5          10          15

Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly
20          25          30

Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His
35          40          45

Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu
50          55          60

Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys
65          70          75          80

Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu
85          90          95

Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser
100         105         110

Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu
115         120         125

Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val
130         135         140

Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp
145         150         155         160

Ser Arg Ile Leu Asp Ser Val Glu Asp Asn Tyr Ile Val Leu Asn Lys
165         170         175

Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly
180         185         190

Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln Phe Val Glu Arg
195         200         205

Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro Thr Ile Cys Lys
210         215         220

Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His Ser Glu Cys Leu
225         230         235         240

```

49321-142 SEQ LIST.txt

Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys Val Ala Cys Arg
245 250 255

Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys Pro Pro Pro Tyr
260 265 270

Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser Phe Cys Gln Asp
275 280 285

Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly Cys His Gln Tyr
290 295 300

Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr
305 310 315 320

Met Asn Ser Ser Asn Leu Leu Cys Thr Pro Cys Leu Gly Pro Cys Pro
325 330 335

Lys Val Cys His Leu Leu Glu Gly Glu Lys Thr Ile Asp Ser Val Thr
340 345 350

Ser Ala Gln Glu Leu Arg Gly Cys Thr Val Ile Asn Gly Ser Leu Ile
355 360 365

Ile Asn Ile Arg Gly Gly Asn Asn Leu Ala Ala Glu Leu Glu Ala Asn
370 375 380

Leu Gly Leu Ile Glu Glu Ile Ser Gly Tyr Leu Lys Ile Arg Arg Ser
385 390 395 400

Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu Arg Leu Ile Arg
405 410 415

Gly Glu Thr Leu Glu Ile Gly Asn Tyr Ser Phe Tyr Ala Leu Asp Asn
420 425 430

Gln Asn Leu Arg Gln Leu Trp Asp Trp Ser Lys His Asn Leu Thr Ile
435 440 445

Thr Gln Gly Lys Leu Phe Phe His Tyr Asn Pro Lys Leu Cys Leu Ser
450 455 460

Glu Ile His Lys Met Glu Glu Val Ser Gly Thr Lys Gly Arg Gln Glu

49321-142 SEQ LIST.txt

```

465                               470                               475                               480

Arg Asn Asp Ile Ala Leu Lys Thr Asn Gly Asp Gln Ala Ser Cys Glu
      485                               490                               495

Asn Glu Leu Leu Lys Phe Ser Tyr Ile Arg Thr Ser Phe Asp Lys Ile
      500                               505                               510

Leu Leu Arg Trp Glu Pro Tyr Trp Pro Pro Asp Phe Arg Asp Leu Leu
      515                               520                               525

Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr Gln Asn Val Thr Glu
      530                               535                               540

Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser Trp Thr Val Val Asp
      545                               550                               555                               560

Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys Ser Gln Asn His Pro
      565                               570                               575

Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr Gln Tyr Ala Ile Phe
      580                               585                               590

Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg Arg Thr Tyr Gly Ala
      595                               600                               605

Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val
      610                               615                               620

Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Ser Gln Ile Ile Leu
      625                               630                               635                               640

Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu
      645                               650                               655

Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp
      660                               665                               670

Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro
      675                               680                               685

Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp
      690                               695                               700

```


49321-142 SEQ LIST.txt

Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu
705 710 715 720

Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu
725 730 735

His Asn Val Val Phe Val Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu
740 745 750

Gly Asp Val Gly Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe
755 760 765

Pro Asn Thr Ser Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg
770 775 780

Pro Phe Glu Lys Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu
785 790 795 800

Arg His Phe Thr Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp
805 810 815

Thr Pro Glu Glu Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr
820 825 830

Met Pro Glu Ala Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu
835 840 845

Ile Phe Glu Asn Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu
850 855 860

Pro Asn Gly Leu Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly
865 870 875 880

Asp Glu Glu Leu His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu
885 890 895

Arg Gly Cys Arg Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg
900 905 910

Ile Arg Ala Thr Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr
915 920 925

Tyr Phe Tyr Val Thr Asp Tyr Leu Asp Val Pro Ser Asn Ile Ala Lys
930 935 940

49321-142 SEQ LIST.txt

Ile Ile Ile Gly Pro Leu Ile Phe Val Phe Leu Phe Ser Val Val Ile
945 950 955 960

Gly Ser Ile Tyr Leu Phe Leu Arg Lys Arg Gln Pro Asp Gly Pro Leu
965 970 975

Gly Pro Leu Tyr Ala Ser Ser Asn Pro Glu Tyr Leu Ser Ala Ser Asp
980 985 990

Val Phe Pro Cys Ser Val Tyr Val Pro Asp Glu Trp Glu Val Ser Arg
995 1000 1005

Glu Lys Ile Thr Leu Leu Arg Glu Leu Gly Gln Gly Ser Phe Gly
1010 1015 1020

Met Val Tyr Glu Gly Asn Ala Arg Asp Ile Ile Lys Gly Glu Ala
1025 1030 1035

Glu Thr Arg Val Ala Val Lys Thr Val Asn Glu Ser Ala Ser Leu
1040 1045 1050

Arg Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Gly
1055 1060 1065

Phe Thr Cys His His Val Val Arg Leu Leu Gly Val Val Ser Lys
1070 1075 1080

Gly Gln Pro Thr Leu Val Val Met Glu Leu Met Ala His Gly Asp
1085 1090 1095

Leu Lys Ser Tyr Leu Arg Ser Leu Arg Pro Glu Ala Glu Asn Asn
1100 1105 1110

Pro Gly Arg Pro Pro Pro Thr Leu Gln Glu Met Ile Gln Met Ala
1115 1120 1125

Ala Glu Ile Ala Asp Gly Met Ala Tyr Leu Asn Ala Lys Lys Phe
1130 1135 1140

Val His Arg Asp Leu Ala Ala Arg Asn Cys Met Val Ala His Asp
1145 1150 1155

Phe Thr Val Lys Ile Gly Asp Phe Gly Met Thr Arg Asp Ile Tyr
1160 1165 1170

49321-142 SEQ LIST.txt

Glu Thr Asp Tyr Tyr Arg Lys Gly Gly Lys Gly Leu Leu Pro Val	
1175	1180 1185
Arg Trp Met Ala Pro Glu Ser Leu Lys Asp Gly Val Phe Thr Thr	
1190	1195 1200
Ser Ser Asp Met Trp Ser Phe Gly Val Val Leu Trp Glu Ile Thr	
1205	1210 1215
Ser Leu Ala Glu Gln Pro Tyr Gln Gly Leu Ser Asn Glu Gln Val	
1220	1225 1230
Leu Lys Phe Val Met Asp Gly Gly Tyr Leu Asp Gln Pro Asp Asn	
1235	1240 1245
Cys Pro Glu Arg Val Thr Asp Leu Met Arg Met Cys Trp Gln Phe	
1250	1255 1260
Asn Pro Asn Met Arg Pro Thr Phe Leu Glu Ile Val Asn Leu Leu	
1265	1270 1275
Lys Asp Asp Leu His Pro Ser Phe Pro Glu Val Ser Phe Phe His	
1280	1285 1290
Ser Glu Glu Asn Lys Ala Pro Glu Ser Glu Glu Leu Glu Met Glu	
1295	1300 1305
Phe Glu Asp Met Glu Asn Val Pro Leu Asp Arg Ser Ser His Cys	
1310	1315 1320
Gln Arg Glu Glu Ala Gly Gly Arg Asp Gly Gly Ser Ser Leu Gly	
1325	1330 1335
Phe Lys Arg Ser Tyr Glu Glu His Ile Pro Tyr Thr His Met Asn	
1340	1345 1350
Gly Gly Lys Lys Asn Gly Arg Ile Leu Thr Leu Pro Arg Ser Asn	
1355	1360 1365
Pro Ser	
1370	

<210> 13

```
<211> 5084
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (22)..(2952)

<220>
<221> variation
<222> (3101)..(3101)
<223> C and T alleles exist at this position
```

```
<220>
<221> variation
<222> (4354)..(4354)
<223> A and G alleles exist at this position
```

```
<220>
<221> variation
<222> (4656)..(4656)
<223> G and T alleles exist at this position
```

```
<400> 13
gatcccatcg cagctaccgc g atg aga ggc gct cgc ggc gcc tgg gat ttt      51
           Met Arg Gly Ala Arg Gly Ala Trp Asp Phe
           1               5               10
```

ctc tgc gtt ctg ctc cta ctg ctt cgc gtc cag aca ggc tct tct caa 99
Leu Cys Val Leu Leu Leu Leu Leu Arg Val Gln Thr Gly Ser Ser Gln
15 20 25

cca tct gtg agt cca ggg gaa ccg tct cca cca tcc atc cat cca gga 147
Pro Ser Val Ser Pro Gly Glu Pro Ser Pro Pro Ser Ile His Pro Gly
30 35 40

aaa tca gac tta ata gtc cgc gtg ggc gac gag att agg ctg tta tgc 195
Lys Ser Asp Leu Ile Val Arg Val Gly Asp Glu Ile Arg Leu Leu Cys
45 50 55

act gat ccg ggc ttt gtc aaa tgg act ttt gag atc ctg gat gaa acg 243
Thr Asp Pro Gly Phe Val Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr
60 65 70

aat gag aat aag cag aat gaa tgg atc acg gaa aag gca gaa gcc acc 291
Asn Glu Asn Lys Gln Asn Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr
75 80 85 90

aac acc ggc aaa tac acg tgc acc aac aaa cac ggc tta agc aat tcc 339
 Asn Thr Gly Lys Tyr Thr Cys Thr Asn Lys His Gly Leu Ser Asn Ser
 95 100 105

att tat gtg ttt gtt aga gat cct gcc aag ctt ttc ctt gtt gac cgc 387
Ile Tyr Val Phe Val Arg Asp Pro Ala Lys Leu Phe Leu Val Asp Arg
110 115 120

tcc ttg tat ggg aaa gaa gac aac gac acg ctg gtc cgc tgt cct ctc 435
Ser Leu Tyr Gly Lys Glu Asp Asn Asp Thr Leu Val Arg Cys Pro Leu

49321-142 SEQ LIST.txt

125	130	135	
aca gac cca gaa gtg acc aat tat tcc ctc aag ggg tgc cag ggg aag Thr Asp Pro Glu Val Thr Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys 140 145 150			483
cct ctt ccc aag gac ttg agg ttt att cct gac ccc aag gcg ggc atc Pro Leu Pro Lys Asp Leu Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile 155 160 165 170			531
atg atc aaa agt gtg aaa cgc gcc tac cat cgg ctc tgt ctg cat tgt Met Ile Lys Ser Val Lys Arg Ala Tyr His Arg Leu Cys Leu His Cys 175 180 185			579
tct gtg gac cag gag ggc aag tca gtg ctg tcg gaa aaa ttc atc ctg Ser Val Asp Gln Glu Gly Lys Ser Val Leu Ser Glu Lys Phe Ile Leu 190 195 200			627
aaa gtg agg cca gcc ttc aaa gct gtg cct gtt gtg tct gtg tcc aaa Lys Val Arg Pro Ala Phe Lys Ala Val Pro Val Val Ser Val Ser Lys 205 210 215			675
gca agc tat ctt ctt agg gaa ggg gaa gaa ttc aca gtg acg tgc aca Ala Ser Tyr Leu Leu Arg Glu Gly Glu Glu Phe Thr Val Thr Cys Thr 220 225 230			723
ata aaa gat gtg tct agt tct gtg tac tca acg tgg aaa aga gaa aac Ile Lys Asp Val Ser Ser Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn 235 240 245 250			771
agt cag act aaa cta cag gag aaa tat aat agc tgg cat cac ggt gac Ser Gln Thr Lys Leu Gln Glu Lys Tyr Asn Ser Trp His His Gly Asp 255 260 265			819
ttc aat tat gaa cgt cag gca acg ttg act atc agt tca gcg aga gtt Phe Asn Tyr Glu Arg Gln Ala Thr Leu Thr Ile Ser Ser Ala Arg Val 270 275 280			867
aat gat tct gga gtg ttc atg tgt tat gcc aat aat act ttt gga tca Asn Asp Ser Gly Val Phe Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser 285 290 295			915
gca aat gtc aca aca acc ttg gaa gta gta gat aaa gga ttc att aat Ala Asn Val Thr Thr Thr Leu Glu Val Val Asp Lys Gly Phe Ile Asn 300 305 310			963
atc ttc ccc atg ata aac act aca gta ttt gta aac gat gga gaa aat Ile Phe Pro Met Ile Asn Thr Thr Val Phe Val Asn Asp Gly Glu Asn 315 320 325 330			1011
gta gat ttg att gtt gaa tat gaa gca ttc ccc aaa cct gaa cac cag Val Asp Leu Ile Val Glu Tyr Glu Ala Phe Pro Lys Pro Glu His Gln 335 340 345			1059
cag tgg atc tat atg aac aga acc ttc act gat aaa tgg gaa gat tat Gln Trp Ile Tyr Met Asn Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr 350 355 360			1107
ccc aag tct gag aat gaa agt aat atc aga tac gta agt gaa ctt cat			1155

49321-142 SEQ LIST.txt

Pro	Lys	Ser	Glu	Asn	Glu	Ser	Asn	Ile	Arg	Tyr	Val	Ser	Glu	Leu	His	
		365					370					375				
cta	acg	aga	tta	aaa	ggc	acc	gaa	gga	ggc	act	tac	aca	ttc	cta	gtg	1203
Leu	Thr	Arg	Leu	Lys	Gly	Thr	Glu	Gly	Gly	Thr	Tyr	Thr	Phe	Leu	Val	
	380					385					390					
tcc	aat	tct	gac	gtc	aat	gct	gcc	ata	gca	ttt	aat	gtt	tat	gtg	aat	1251
Ser	Asn	Ser	Asp	Val	Asn	Ala	Ala	Ile	Ala	Phe	Asn	Val	Tyr	Val	Asn	
395					400					405					410	
aca	aaa	cca	gaa	atc	ctg	act	tac	gac	agg	ctc	gtg	aat	ggc	atg	ctc	1299
Thr	Lys	Pro	Glu	Ile	Leu	Thr	Tyr	Asp	Arg	Leu	Val	Asn	Gly	Met	Leu	
				415					420					425		
caa	tgt	gtg	gca	gca	gga	ttc	cca	gag	ccc	aca	ata	gat	tgg	tat	ttt	1347
Gln	Cys	Val	Ala	Ala	Gly	Phe	Pro	Glu	Pro	Thr	Ile	Asp	Trp	Tyr	Phe	
			430					435					440			
tgt	cca	gga	act	gag	cag	aga	tgc	tct	gct	tct	gta	ctg	cca	gtg	gat	1395
Cys	Pro	Gly	Thr	Glu	Gln	Arg	Cys	Ser	Ala	Ser	Val	Leu	Pro	Val	Asp	
	445						450					455				
gtg	cag	aca	cta	aac	tca	tct	ggg	cca	ccg	ttt	gga	aag	cta	gtg	gtt	1443
Val	Gln	Thr	Leu	Asn	Ser	Ser	Gly	Pro	Pro	Phe	Gly	Lys	Leu	Val	Val	
	460					465					470					
cag	agt	tct	ata	gat	tct	agt	gca	ttc	aag	cac	aat	ggc	acg	gtt	gaa	1491
Gln	Ser	Ser	Ile	Asp	Ser	Ser	Ala	Phe	Lys	His	Asn	Gly	Thr	Val	Glu	
475					480					485					490	
tgt	aag	gct	tac	aac	gat	gtg	ggc	aag	act	tct	gcc	tat	ttt	aac	ttt	1539
Cys	Lys	Ala	Tyr	Asn	Asp	Val	Gly	Lys	Thr	Ser	Ala	Tyr	Phe	Asn	Phe	
				495					500					505		
gca	ttt	aaa	ggg	aac	aac	aaa	gag	caa	atc	cat	ccc	cac	acc	ctg	ttc	1587
Ala	Phe	Lys	Gly	Asn	Asn	Lys	Glu	Gln	Ile	His	Pro	His	Thr	Leu	Phe	
			510					515					520			
act	cct	ttg	ctg	att	ggg	ttc	gta	atc	gta	gct	ggc	atg	atg	tgc	att	1635
Thr	Pro	Leu	Leu	Ile	Gly	Phe	Val	Ile	Val	Ala	Gly	Met	Met	Cys	Ile	
		525					530					535				
att	gtg	atg	att	ctg	acc	tac	aaa	tat	tta	cag	aaa	ccc	atg	tat	gaa	1683
Ile	Val	Met	Ile	Leu	Thr	Tyr	Lys	Tyr	Leu	Gln	Lys	Pro	Met	Tyr	Glu	
	540					545					550					
gta	cag	tgg	aag	gtt	gtt	gag	gag	ata	aat	gga	aac	aat	tat	gtt	tac	1731
Val	Gln	Trp	Lys	Val	Val	Glu	Glu	Ile	Asn	Gly	Asn	Asn	Tyr	Val	Tyr	
555					560					565					570	
ata	gac	cca	aca	caa	ctt	cct	tat	gat	cac	aaa	tgg	gag	ttt	ccc	aga	1779
Ile	Asp	Pro	Thr	Gln	Leu	Pro	Tyr	Asp	His	Lys	Trp	Glu	Phe	Pro	Arg	
				575					580					585		
aac	agg	ctg	agt	ttt	ggg	aaa	acc	ctg	ggg	gct	gga	gct	ttc	ggg	aag	1827
Asn	Arg	Leu	Ser	Phe	Gly	Lys	Thr	Leu	Gly	Ala	Gly	Ala	Phe	Gly	Lys	
			590					595					600			

49321-142 SEQ LIST.txt

gtt gtt gag gca act gct tat ggc tta att aag tca gat gcg gcc atg Val Val Glu Ala Thr Ala Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met 605 610 615	1875
act gtc gct gta aag atg ctc aag ccg agt gcc cat ttg aca gaa cgg Thr Val Ala Val Lys Met Leu Lys Pro Ser Ala His Leu Thr Glu Arg 620 625 630	1923
gaa gcc ctc atg tct gaa ctc aaa gtc ctg agt tac ctt ggt aat cac Glu Ala Leu Met Ser Glu Leu Lys Val Leu Ser Tyr Leu Gly Asn His 635 640 645 650	1971
atg aat att gtg aat cta ctt gga gcc tgc acc att gga ggg ccc acc Met Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr 655 660 665	2019
ctg gtc att aca gaa tat tgt tgc tat ggt gat ctt ttg aat ttt ttg Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu 670 675 680	2067
aga aga aaa cgt gat tca ttt att tgt tca aag cag gaa gat cat gca Arg Arg Lys Arg Asp Ser Phe Ile Cys Ser Lys Gln Glu Asp His Ala 685 690 695	2115
gaa gct gca ctt tat aag aat ctt ctg cat tca aag gag tct tcc tgc Glu Ala Ala Leu Tyr Lys Asn Leu Leu His Ser Lys Glu Ser Ser Cys 700 705 710	2163
agc gat agt act aat gag tac atg gac atg aaa cct gga gtt tct tat Ser Asp Ser Thr Asn Glu Tyr Met Asp Met Lys Pro Gly Val Ser Tyr 715 720 725 730	2211
gtt gtc cca acc aag gcc gac aaa agg aga tct gtg aga ata ggc tca Val Val Pro Thr Lys Ala Asp Lys Arg Arg Ser Val Arg Ile Gly Ser 735 740 745	2259
tac ata gaa aga gat gtg act ccc gcc atc atg gag gat gac gag ttg Tyr Ile Glu Arg Asp Val Thr Pro Ala Ile Met Glu Asp Asp Glu Leu 750 755 760	2307
gcc cta gac tta gaa gac ttg ctg agc ttt tct tac cag gtg gca aag Ala Leu Asp Leu Glu Asp Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys 765 770 775	2355
ggc atg gct ttc ctc gcc tcc aag aat tgt att cac aga gac ttg gca Gly Met Ala Phe Leu Ala Ser Lys Asn Cys Ile His Arg Asp Leu Ala 780 785 790	2403
gcc aga aat atc ctc ctt act cat ggt cgg atc aca aag att tgt gat Ala Arg Asn Ile Leu Leu Thr His Gly Arg Ile Thr Lys Ile Cys Asp 795 800 805 810	2451
ttt ggt cta gcc aga gac atc aag aat gat tct aat tat gtg gtt aaa Phe Gly Leu Ala Arg Asp Ile Lys Asn Asp Ser Asn Tyr Val Val Lys 815 820 825	2499
gga aac gct cga cta cct gtg aag tgg atg gca cct gaa agc att ttc Gly Asn Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe 830 835 840	2547

49321-142 SEQ LIST.txt

aac tgt gta tac acg ttt gaa agt gac gtc tgg tcc tat ggg att ttt Asn Cys Val Tyr Thr Phe Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe 845 850 855	2595
ctt tgg gag ctg ttc tct tta gga agc agc ccc tat cct gga atg ccg Leu Trp Glu Leu Phe Ser Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro 860 865 870	2643
gtc gat tct aag ttc tac aag atg atc aag gaa ggc ttc cgg atg ctc Val Asp Ser Lys Phe Tyr Lys Met Ile Lys Glu Gly Phe Arg Met Leu 875 880 885 890	2691
agc cct gaa cac gca cct gct gaa atg tat gac ata atg aag act tgc Ser Pro Glu His Ala Pro Ala Glu Met Tyr Asp Ile Met Lys Thr Cys 895 900 905	2739
tgg gat gca gat ccc cta aaa aga cca aca ttc aag caa att gtt cag Trp Asp Ala Asp Pro Leu Lys Arg Pro Thr Phe Lys Gln Ile Val Gln 910 915 920	2787
cta att gag aag cag att tca gag agc acc aat cat att tac tcc aac Leu Ile Glu Lys Gln Ile Ser Glu Ser Thr Asn His Ile Tyr Ser Asn 925 930 935	2835
tta gca aac tgc agc ccc aac cga cag aag ccc gtg gta gac cat tct Leu Ala Asn Cys Ser Pro Asn Arg Gln Lys Pro Val Val Asp His Ser 940 945 950	2883
gtg cgg atc aat tct gtc ggc agc acc gct tcc tcc tcc cag cct ctg Val Arg Ile Asn Ser Val Gly Ser Thr Ala Ser Ser Ser Gln Pro Leu 955 960 965 970	2931
ctt gtg cac gac gat gtc tga gcagaatcag tgtttgggtc acccctccag Leu Val His Asp Asp Val 975	2982
gaatgatctc ttcttttggc ttccatgatg gttatttttct tttctttcaa cttgcatcca	3042
actccaggat agtgggcacc ccaactgcaat cctgtctttc tgagcacact ttagtggcyg	3102
atgatttttg tcatcagcca ccacctatt gcaaagggtc caactgtata tattcccaat	3162
agcaacgtag cttctacat gaacagaaaa cattctgatt tggaaaaaga gagggaggtg	3222
tggactgggg gccagagtcc tttccaaggc ttctccaatt ctgccccaaa atatggttga	3282
tagtttacct gaataaatgg tagtaatcac agttggcctt cagaaccatc catagtagta	3342
tgatgataca agattagaag ctgaaaacct aagtccttta tgtggaaaac agaacatcat	3402
tagaacaaag gacagagtat gaacacctgg gcttaagaaa tctagtattt catgctggga	3462
atgagacata ggccatgaaa aaaatgatcc ccaagtgtga acaaaagatg ctcttctgtg	3522
gaccactgca tgagctttta tactaccgac ctggttttta aatagagttt gctattagag	3582
cattgaattg gagagaaggc ctccctagcc agcacttgta tatacgcac tataaattgt	3642

49321-142 SEQ LIST.txt

ccgtgttcat acatttgagg ggaaaacacc ataaggtttc gtttctgtat acaaccctgg	3702
cattatgtcc actgtgtata gaagtagatt aagagccata taagtttgaa ggaaacagtt	3762
aataccattt ttttaaggaaa caatataacc acaaagcaca gtttgaacaa aatctcctct	3822
tttagctgat gaacttattc tgtagattct gtggaacaag cctatcagct tcagaatggc	3882
attgtactca atggatttga tgctgtttga caaagttact gattcactgc atggctccca	3942
caggagtggg aaaacactgc catcttagtt tggattctta tgtagcagga aataaagtat	4002
aggtttagcc tccttcgcag gcatgtcctg gacaccgggc cagtatctat atatgtgtat	4062
gtacgtttgt atgtgtgtag acaaatattt ggaggggtat ttttgcctg agtccaagag	4122
ggtcctttag tacctgaaaa gtaacttggc tttcattatt agtactgctc ttgtttcttt	4182
tcacatagct gtctagagta gcttaccaga agcttccata gtggtgcaga ggaagtggaa	4242
ggcatcagtc cctatgtatt tgcagttcac ctgcacttaa ggcactctgt tatttagact	4302
catcttactg tacctgttcc ttagaccttc cataatgcta ctgtctcact graacattta	4362
aattttaccc ttttagactgt agcctggata ttattcttgt agtttacctc tttaaaaaca	4422
aaacaaaaca aaacaaaaaa ctccccttcc tctactgcca atataaaagg caaatgtgta	4482
catggcagag tttgtgtgtt gtcttgaaag attcaggtat gttgccttta tggtttcccc	4542
cttctacatt tcttagacta catttagaga actgtggccg ttatctggaa gtaaccattt	4602
gcactggagt tctatgctct cgcaccttcc caaagttaac agattttggg gttktgttgt	4662
cacccaagag attgttgttt gccatacttt gtctgaaaaa ttcctttgtg tttctattga	4722
cttcaatgat agtaagaaaa gtggttggtta gttatagatg tctaggtact tcaggggcac	4782
ttcattgaga gttttgtctt gccatacttt gtctgaaaaa ttcctttgtg tttctattga	4842
cttcaatgat agtaagaaaa gtggttggtta gttatagatg tctaggtact tcaggggcac	4902
ttcattgaga gttttgtcaa tgtcttttga atattcccaa gcccatgagt ccttgaaaat	4962
atTTTTtata tatacagtaa ctttatgtgt aaatacataa gcggcgtaag tttaaaggat	5022
gttgggtgttc cacgtgtttt attcctgtat gttgtccaat tgttgacagt tctgaagaat	5082
tc	5084

<210> 14
 <211> 976
 <212> PRT
 <213> Homo sapiens

<400> 14

Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Leu Cys Val Leu Leu Leu

49321-142 SEQ LIST.txt

```

1              5              10              15

Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pro Ser Val Ser Pro Gly
      20              25              30

Glu Pro Ser Pro Pro Ser Ile His Pro Gly Lys Ser Asp Leu Ile Val
      35              40              45

Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Thr Asp Pro Gly Phe Val
      50              55              60

Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr Asn Glu Asn Lys Gln Asn
      65              70              75              80

Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr Asn Thr Gly Lys Tyr Thr
      85              90              95

Cys Thr Asn Lys His Gly Leu Ser Asn Ser Ile Tyr Val Phe Val Arg
      100             105             110

Asp Pro Ala Lys Leu Phe Leu Val Asp Arg Ser Leu Tyr Gly Lys Glu
      115             120             125

Asp Asn Asp Thr Leu Val Arg Cys Pro Leu Thr Asp Pro Glu Val Thr
      130             135             140

Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys Pro Leu Pro Lys Asp Leu
      145             150             155             160

Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile Met Ile Lys Ser Val Lys
      165             170             175

Arg Ala Tyr His Arg Leu Cys Leu His Cys Ser Val Asp Gln Glu Gly
      180             185             190

Lys Ser Val Leu Ser Glu Lys Phe Ile Leu Lys Val Arg Pro Ala Phe
      195             200             205

Lys Ala Val Pro Val Val Ser Val Ser Lys Ala Ser Tyr Leu Leu Arg
      210             215             220

Glu Gly Glu Glu Phe Thr Val Thr Cys Thr Ile Lys Asp Val Ser Ser
      225             230             235             240

```

49321-142 SEQ LIST.txt

Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn Ser Gln Thr Lys Leu Gln
 245 250 255

Glu Lys Tyr Asn Ser Trp His His Gly Asp Phe Asn Tyr Glu Arg Gln
 260 265 270

Ala Thr Leu Thr Ile Ser Ser Ala Arg Val Asn Asp Ser Gly Val Phe
 275 280 285

Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser Ala Asn Val Thr Thr Thr
 290 295 300

Leu Glu Val Val Asp Lys Gly Phe Ile Asn Ile Phe Pro Met Ile Asn
 305 310 315 320

Thr Thr Val Phe Val Asn Asp Gly Glu Asn Val Asp Leu Ile Val Glu
 325 330 335

Tyr Glu Ala Phe Pro Lys Pro Glu His Gln Gln Trp Ile Tyr Met Asn
 340 345 350

Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr Pro Lys Ser Glu Asn Glu
 355 360 365

Ser Asn Ile Arg Tyr Val Ser Glu Leu His Leu Thr Arg Leu Lys Gly
 370 375 380

Thr Glu Gly Gly Thr Tyr Thr Phe Leu Val Ser Asn Ser Asp Val Asn
 385 390 395 400

Ala Ala Ile Ala Phe Asn Val Tyr Val Asn Thr Lys Pro Glu Ile Leu
 405 410 415

Thr Tyr Asp Arg Leu Val Asn Gly Met Leu Gln Cys Val Ala Ala Gly
 420 425 430

Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe Cys Pro Gly Thr Glu Gln
 435 440 445

Arg Cys Ser Ala Ser Val Leu Pro Val Asp Val Gln Thr Leu Asn Ser
 450 455 460

Ser Gly Pro Pro Phe Gly Lys Leu Val Val Gln Ser Ser Ile Asp Ser
 465 470 475 480

49321-142 SEQ LIST.txt

Ser Ala Phe Lys His Asn Gly Thr Val Glu Cys Lys Ala Tyr Asn Asp
 485 490 495
 Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe Ala Phe Lys Gly Asn Asn
 500 505 510
 Lys Glu Gln Ile His Pro His Thr Leu Phe Thr Pro Leu Leu Ile Gly
 515 520 525
 Phe Val Ile Val Ala Gly Met Met Cys Ile Ile Val Met Ile Leu Thr
 530 535 540
 Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Val Gln Trp Lys Val Val
 545 550 555 560
 Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr Ile Asp Pro Thr Gln Leu
 565 570 575
 Pro Tyr Asp His Lys Trp Glu Phe Pro Arg Asn Arg Leu Ser Phe Gly
 580 585 590
 Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys Val Val Glu Ala Thr Ala
 595 600 605
 Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met Thr Val Ala Val Lys Met
 610 615 620
 Leu Lys Pro Ser Ala His Leu Thr Glu Arg Glu Ala Leu Met Ser Glu
 625 630 635 640
 Leu Lys Val Leu Ser Tyr Leu Gly Asn His Met Asn Ile Val Asn Leu
 645 650 655
 Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr Leu Val Ile Thr Glu Tyr
 660 665 670
 Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu Arg Arg Lys Arg Asp Ser
 675 680 685
 Phe Ile Cys Ser Lys Gln Glu Asp His Ala Glu Ala Ala Leu Tyr Lys
 690 695 700
 Asn Leu Leu His Ser Lys Glu Ser Ser Cys Ser Asp Ser Thr Asn Glu
 705 710 715 720

49321-142 SEQ LIST.txt

Tyr Met Asp Met Lys Pro Gly Val Ser Tyr Val Val Pro Thr Lys Ala
 725 730 735
 Asp Lys Arg Arg Ser Val Arg Ile Gly Ser Tyr Ile Glu Arg Asp Val
 740 745 750
 Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Ala Leu Asp Leu Glu Asp
 755 760 765
 Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys Gly Met Ala Phe Leu Ala
 770 775 780
 Ser Lys Asn Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu
 785 790 795 800
 Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp
 805 810 815
 Ile Lys Asn Asp Ser Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro
 820 825 830
 Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Cys Val Tyr Thr Phe
 835 840 845
 Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe Leu Trp Glu Leu Phe Ser
 850 855 860
 Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro Val Asp Ser Lys Phe Tyr
 865 870 875 880
 Lys Met Ile Lys Glu Gly Phe Arg Met Leu Ser Pro Glu His Ala Pro
 885 890 895
 Ala Glu Met Tyr Asp Ile Met Lys Thr Cys Trp Asp Ala Asp Pro Leu
 900 905 910
 Lys Arg Pro Thr Phe Lys Gln Ile Val Gln Leu Ile Glu Lys Gln Ile
 915 920 925
 Ser Glu Ser Thr Asn His Ile Tyr Ser Asn Leu Ala Asn Cys Ser Pro
 930 935 940
 Asn Arg Gln Lys Pro Val Val Asp His Ser Val Arg Ile Asn Ser Val

49321-142 SEQ LIST.txt

```

<220>
<223> Neuritin-specific PMO antisense oligonucleotide

<400> 19
ttaactccca tcctacgttt agtca 25

<210> 20
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> INSR-specific PMO antisense oligonucleotide

<400> 20
gggtctcctc ggatcaggcg cg 22

<210> 21
<211> 23
<212> DNA
<213> artificial sequence

<220>
<223> KIT-specific PMO antisense oligonucleotide

<400> 21
cgcctctcat cgcggtagct gcg 23

<210> 22
<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> IFACTOR-specific PMO antisense oligonucleotide

<400> 22
agcttcatgt tggagggtgtt cg 22

<210> 23
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> LMO2-specific PMO antisense oligonucleotide

<400> 23
gccgaggaca ttggggaggag aggcg 25

<210> 24
<211> 25
<212> DNA

```

49321-142 SEQ LIST.txt

<213> artificial sequence

<220>

<223> MFAP3-specific PMO antisense oligonucleotide

<400> 24

tgaataagca acaatgtagc ttcac

25

<210> 25

<211> 1946

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (274)..(1527)

<400> 25

agacactgcc cgctctccgg gactccgcgc cgctccccgt tgccttccag gactgagaaa 60

ggggaaaggg aaggggtgcca cgtccgagca gccgccttga ctggggaagg gtctgaatcc 120

cacccttggc attgcttggg ggagactgag ataccctgac tccgctcgcc tccttggttg 180

aagatttctc cttccctcac gtgatttgag ccccggtttt attttctgtg agccacgtcc 240

tcctcgagcg ggggtcaatct ggcaaaagga gtg atg cgc ttc gcc tgg acc gtg 294
Met Arg Phe Ala Trp Thr Val
1 5

ctc ctg ctc ggg cct ttg cag ctc tgc gcg cta gtg cac tgc gcc cct 342
Leu Leu Leu Gly Pro Leu Gln Leu Cys Ala Leu Val His Cys Ala Pro
10 15 20

ccc gcc gcc ggc caa cag cag ccc ccg cgc gag ccg ccg gcg gct ccg 390
Pro Ala Ala Gly Gln Gln Gln Pro Pro Arg Glu Pro Pro Ala Ala Pro
25 30 35

ggc gcc tgg cgc cag cag atc caa tgg gag aac aac ggg cag gtg ttc 438
Gly Ala Trp Arg Gln Gln Ile Gln Trp Glu Asn Asn Gly Gln Val Phe
40 45 50 55

agc ttg ctg agc ctg ggc tca cag tac cag cct cag cgc cgc cgg gac 486
Ser Leu Leu Ser Leu Gly Ser Gln Tyr Gln Pro Gln Arg Arg Arg Asp
60 65 70

ccg ggc gcc gcc gtc cct ggt gca gcc aac gcc tcc gcc cag cag ccc 534
Pro Gly Ala Ala Val Pro Gly Ala Ala Asn Ala Ser Ala Gln Gln Pro
75 80 85

cgc act ccg atc ctg ctg atc cgc gac aac cgc acc gcc gcg gcg cga 582
Arg Thr Pro Ile Leu Leu Ile Arg Asp Asn Arg Thr Ala Ala Ala Arg
90 95 100

acg cgg acg gcc ggc tca tct gga gtc acc gct ggc cgc ccc agg ccc 630
Thr Arg Thr Ala Gly Ser Ser Gly Val Thr Ala Gly Arg Pro Arg Pro
105 110 115

49321-142 SEQ LIST.txt

acc gcc cgt cac tgg ttc caa gct ggc tac tcg aca tct aga gcc cgc Thr Ala Arg His Trp Phe Gln Ala Gly Tyr Ser Thr Ser Arg Ala Arg 120 125 130 135	678
gaa gct ggc gcc tcg cgc gcg gag aac cag aca gcg ccg gga gaa gtt Glu Ala Gly Ala Ser Arg Ala Glu Asn Gln Thr Ala Pro Gly Glu Val 140 145 150	726
cct gcg ctc agt aac ctg cgg ccg ccc agc cgc gtg gac ggc atg gtg Pro Ala Leu Ser Asn Leu Arg Pro Pro Ser Arg Val Asp Gly Met Val 155 160 165	774
ggc gac gac cct tac aac ccc tac aag tac tct gac gac aac cct tat Gly Asp Asp Pro Tyr Asn Pro Tyr Lys Tyr Ser Asp Asp Asn Pro Tyr 170 175 180	822
tac aac tac tac gat act tat gaa agg ccc aga cct ggg ggc agg tac Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg Pro Arg Pro Gly Gly Arg Tyr 185 190 195	870
cgg ccc gga tac ggc act ggc tac ttc cag tac ggt ctc cca gac ctg Arg Pro Gly Tyr Gly Thr Gly Tyr Phe Gln Tyr Gly Leu Pro Asp Leu 200 205 210 215	918
gtg gcc gac ccc tac tac atc cag gcg tcc acg tac gtg cag aag atg Val Ala Asp Pro Tyr Tyr Ile Gln Ala Ser Thr Tyr Val Gln Lys Met 220 225 230	966
tcc atg tac aac ctg aga tgc gcg gcg gag gaa aac tgt ctg gcc agt Ser Met Tyr Asn Leu Arg Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser 235 240 245	1014
aca gca tac agg gca gat gtc aga gat tat gat cac agg gtg ctg ctc Thr Ala Tyr Arg Ala Asp Val Arg Asp Tyr Asp His Arg Val Leu Leu 250 255 260	1062
aga ttt ccc caa aga gtg aaa aac caa ggg aca tca gat ttc tta ccc Arg Phe Pro Gln Arg Val Lys Asn Gln Gly Thr Ser Asp Phe Leu Pro 265 270 275	1110
agc cga cca aga tat tcc tgg gaa tgg cac agt tgt cat caa cat tac Ser Arg Pro Arg Tyr Ser Trp Glu Trp His Ser Cys His Gln His Tyr 280 285 290 295	1158
cac agt atg gat gag ttt agc cac tat gac ctg ctt gat gcc aac acc His Ser Met Asp Glu Phe Ser His Tyr Asp Leu Leu Asp Ala Asn Thr 300 305 310	1206
cag agg aga gtg gct gaa ggc cac aaa gca agt ttc tgt ctt gaa gac Gln Arg Arg Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp 315 320 325	1254
aca tcc tgt gac tat ggc tac cac agg cga ttt gca tgt act gca cac Thr Ser Cys Asp Tyr Gly Tyr His Arg Arg Phe Ala Cys Thr Ala His 330 335 340	1302
aca cag gga ttg agt cct ggc tgt tat gat acc tat ggt gca gac ata Thr Gln Gly Leu Ser Pro Gly Cys Tyr Asp Thr Tyr Gly Ala Asp Ile	1350

49321-142 SEQ LIST.txt

```

345                               350                               355
gac tgc cag tgg att gat att aca gat gta aaa cct gga aac tat atc      1398
Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr Ile
360                               365                               370                               375

cta aag gtc agt gta aac ccc agc tac ctg gtt cct gaa tct gac tat      1446
Leu Lys Val Ser Val Asn Pro Ser Tyr Leu Val Pro Glu Ser Asp Tyr
                               380                               385                               390

acc aac aat gtt gtg cgc tgt gac att cgc tac aca gga cat cat gcg      1494
Thr Asn Asn Val Val Arg Cys Asp Ile Arg Tyr Thr Gly His His Ala
                               395                               400                               405

tat gcc tca ggc tgc aca att tca ccg tat tag aaggcaaagc aaaactccca      1547
Tyr Ala Ser Gly Cys Thr Ile Ser Pro Tyr
                               410                               415

atggataaat cagtgcctgg tggtctgaag tgggaaaaaa tagactaact tcagtaggat      1607

ttatgtatatt tgaaaaagag aacagaaaac aacaaaagaa tttttgtttg gactgttttc      1667

aataacaaag cacataactg gattttgaac gcttaagtca tcattacttg ggaaattttt      1727

aatgtttatt atttacatca ctttgtgaat taacacagtg tttcaattct gtaattacat      1787

atgtgactct ttcaaagaaa tccaaatttc tcatgttcct tttgaaattg tagtgcaaaa      1847

tggtcagtat tatctaaatg aatgagccaa aatgactttg aactgaaact tttctaaagt      1907

gctggaactt tagtgaaaca taataataat ggggtttata      1946

<210> 26
<211> 417
<212> PRT
<213> Homo sapiens

<400> 26

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
1                               5                               10                               15

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
20                               25                               30

Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp
35                               40                               45

Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
50                               55                               60

Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
65                               70                               75                               80

```

49321-142 SEQ LIST.txt

Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
85 90 95

Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
100 105 110

Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
115 120 125

Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Ala Ser Arg Ala Glu Asn
130 135 140

Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro
145 150 155 160

Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
165 170 175

Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
180 185 190

Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
195 200 205

Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
210 215 220

Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
225 230 235 240

Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
245 250 255

Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
260 265 270

Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp
275 280 285

His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr
290 295 300

Asp Leu Leu Asp Ala Asn Thr Gln Arg Arg Val Ala Glu Gly His Lys
305 310 315 320

49321-142 SEQ LIST.txt

Ala Ser Phe Cys Leu Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg
 325 330 335

Arg Phe Ala Cys Thr Ala His Thr Gln Gly Leu Ser Pro Gly Cys Tyr
 340 345 350

Asp Thr Tyr Gly Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp
 355 360 365

Val Lys Pro Gly Asn Tyr Ile Leu Lys Val Ser Val Asn Pro Ser Tyr
 370 375 380

Leu Val Pro Glu Ser Asp Tyr Thr Asn Asn Val Val Arg Cys Asp Ile
 385 390 395 400

Arg Tyr Thr Gly His His Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro
 405 410 415

Tyr

<210> 27
 <211> 2389
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(1146)

<400> 27
 ggggaaggcga gcagtgccaa tctacagcga agaaagtctc gtttggtaaa agcgagaggg 60
 gaaagcctga gc atg cag agt gtg cag agc acg agc ttt tgt ctc cga aag 111
 Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys
 1 5 10
 cag tgc ctt tgc ctg acc ttc ctg ctt ctc cat ctc ctg gga cag gtc 159
 Gln Cys Leu Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val
 15 20 25
 gct gcg act cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg 207
 Ala Ala Thr Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala
 30 35 40 45
 acg ccg ccg acc tgc gcc ccc ggg gtg cgc gcg gtg ctg gac ggc tgc 255
 Thr Pro Pro Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys
 50 55 60

49321-142 SEQ LIST.txt

tca tgc tgt ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat	303
Ser Cys Cys Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp	
65 70 75	
ctg gag cca tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg	351
Leu Glu Pro Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala	
80 85 90	
gac ccc agc aac cag act ggc atc tgc acg gcg gta gag gga gat aac	399
Asp Pro Ser Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn	
95 100 105	
tgt gtg ttc gat ggg gtc atc tac cgc agt gga gag aaa ttt cag cca	447
Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro	
110 115 120 125	
agc tgc aaa ttc cag tgc acc tgc aga gat ggg cag att ggc tgt gtg	495
Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val	
130 135 140	
ccc cgc tgt cag ctg gat gtg cta ctg cct gag cct aac tgc cca gct	543
Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala	
145 150 155	
cca aga aaa gtt gag gtg cct gga gag tgc tgt gaa aag tgg atc tgt	591
Pro Arg Lys Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys	
160 165 170	
ggc cca gat gag gag gat tca ctg gga ggc ctt acc ctt gca gct tac	639
Gly Pro Asp Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr	
175 180 185	
agg cca gaa gcc acc cta gga gta gaa gtc tct gac tca agt gtc aac	687
Arg Pro Glu Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn	
190 195 200 205	
tgc att gaa cag acc aca gag tgg aca gca tgc tcc aag agc tgt ggt	735
Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly	
210 215 220	
atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt gag atg	783
Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met	
225 230 235	
ctg aaa cag act cgg ctc tgc atg gtg cgg ccc tgt gaa caa gag cca	831
Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro	
240 245 250	
gag cag cca aca gat aag aaa gga aaa aag tgt ctc cgc acc aag aag	879
Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys	
255 260 265	
tca ctc aaa gcc atc cac ctg cag ttc aag aac tgc acc agc ctg cac	927
Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His	
270 275 280 285	
acc tac aag ccc agg ttc tgt ggg gtc tgc agt gat ggc cgc tgc tgc	975
Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys	
290 295 300	

49321-142 SEQ LIST.txt

act ccc cac aat acc aaa acc atc cag gca gag ttt cag tgc tcc cca	1023
Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro	
305 310 315	
ggg caa ata gtc aag aag cca gtg atg gtc att ggg acc tgc acc tgt	1071
Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys	
320 325 330	
cac acc aac tgt cct aag aac aat gag gcc ttc ctc cag gag ctg gag	1119
His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu	
335 340 345	
ctg aag act acc aga ggg aaa atg taa cctatcactc aagaagcaca	1166
Leu Lys Thr Thr Arg Gly Lys Met	
350 355	
cctacagagc acctgtagct gctgcgccac ccaccatcaa aggaatataa gaaaagtaat	1226
gaagaatcac gatttcatcc ttgaatccta tgtattttcc taatgtgatc atatgaggac	1286
ctttcatatc tgtctttttat ttaacaaaaa atgtaattaa ctgtaaactt ggaatcaagg	1346
taagctcagg atatggctta ggaatgactt actttcctgt ggttttatta caaatgcaaa	1406
tttctataaa ttttaagaaaa caagtatata atttactttg tagactgttt cacattgcac	1466
tcatcatatt ttgttgtgca ctagtgcaat tccaagaaaa tatcactgta atgagtcagt	1526
gaagtctaga atcatactta acatttcatt gtacaagtat tacaaccata tattgaggtt	1586
cattgggaag attctctatt ggctcccttt ttgggtaaac cagctctgaa cttccaagct	1646
ccaaatccaa ggaaacatgc agctcttcaa catgacatcc agagatgact attacttttc	1706
tgtttagttt tacactagga aacgtgttgt atctacagta atgaaatgtt tactaagtgg	1766
actggtgtca taaactttct ccatttaaga cacattgact cttttccaat agaaagaaac	1826
taaacagaaa actcccaata caaagatgac tggtcctca tagccctcag acatttatat	1886
attggaagct gctgaggccc ccaagttttt taattaagca gaaacagcat attagcaggg	1946
attctctcat ctaactgatg agtaaactga ggcccaaagc acttgcttac atcctctgat	2006
agctgtttca aatgtgcatt ttgtggaatt ttgagaaaaa tagagcaaaa tcaacatgac	2066
tggtggtgag agaccacaca ttttatgaga gtttggaatt attgtagaca tgcccaaaac	2126
ttatccttgg gccataatta tgaaaactca tgatcaagat atatgtgtat acatacatgt	2186
atctggtttg tcaggctaca aggtaggctg caaaattaaa tctagacatt cttttaatgc	2246
caccacacgt gttccgcttc tctcttttaa agtatttata aaaatataaa ttgtacattt	2306
tgtaaaatat tatgtttgat ttctctactt gtcatatcac taaataaaca cgattttatt	2366
gctgaaaaaa aaaaaaaaaa aaa	2389

49321-142 SEQ LIST.txt

<210> 28
 <211> 357
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys Gln Cys Leu
 1 5 10 15

Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val Ala Ala Thr
 20 25 30

Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro
 35 40 45

Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys
 50 55 60

Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro
 65 70 75 80

Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser
 85 90 95

Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn Cys Val Phe
 100 105 110

Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys
 115 120 125

Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys
 130 135 140

Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys
 145 150 155 160

Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp
 165 170 175

Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu
 180 185 190

Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn Cys Ile Glu
 195 200 205

49321-142 SEQ LIST.txt

Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe
210 215 220

Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln
225 230 235 240

Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro Glu Gln Pro
245 250 255

Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys
260 265 270

Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His Thr Tyr Lys
275 280 285

Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His
290 295 300

Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro Gly Gln Ile
305 310 315 320

Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn
325 330 335

Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu Leu Lys Thr
340 345 350

Thr Arg Gly Lys Met
355

<210> 29
<211> 1518
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (22) .. (1503)

<400> 29
aaccaccatt ttgcaaggac c atg agg cca ctg tgc gtg aca tgc tgg tgg 51
Met Arg Pro Leu Cys Val Thr Cys Trp Trp
1 5 10

ctc gga ctg ctg gct gcc atg gga gct gtt gca ggc cag gag gac ggt 99
Leu Gly Leu Leu Ala Ala Met Gly Ala Val Ala Gly Gln Glu Asp Gly
15 20 25

49321-142 SEQ LIST.txt

ttt gag ggc act gag gag ggc tcg cca aga gag ttc att tac cta aac	147
Phe Glu Gly Thr Glu Glu Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn	
30 35 40	
agg tac aag cgg gcg ggc gag tcc cag gac aag tgc acc tac acc ttc	195
Arg Tyr Lys Arg Ala Gly Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe	
45 50 55	
att gtg ccc cag cag cgg gtc acg ggt gcc atc tgc gtc aac tcc aag	243
Ile Val Pro Gln Gln Arg Val Thr Gly Ala Ile Cys Val Asn Ser Lys	
60 65 70	
gag cct gag gtg ctt ctg gag aac cga gtg cat aag cag gag cta gag	291
Glu Pro Glu Val Leu Leu Glu Asn Arg Val His Lys Gln Glu Leu Glu	
75 80 85 90	
ctg ctc aac aat gag ctg ctc aag cag aag cgg cag atc gag aca ctg	339
Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu	
95 100 105	
cag cag ctg gtg gag gtg gac ggc ggc att gtg agc gag gtg aag ctg	387
Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu Val Lys Leu	
110 115 120	
ctg cgc aag gag agc cgc aac atg aac tcg cgg gtc acg cag ctc tac	435
Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr	
125 130 135	
atg cag ctc ctg cac gag atc atc cgc aag cgg gac aac gcg ttg gag	483
Met Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ala Leu Glu	
140 145 150	
ctc tcc cag ctg gag aac agg atc ctg aac cag aca gcc gac atg ctg	531
Leu Ser Gln Leu Glu Asn Arg Ile Leu Asn Gln Thr Ala Asp Met Leu	
155 160 165 170	
cag ctg gcc agc aag tac aag gac ctg gag cac aag tac cag cac ctg	579
Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu His Lys Tyr Gln His Leu	
175 180 185	
gcc aca ctg gcc cac aac caa tca gag atc atc gcg cag ctt gag gag	627
Ala Thr Leu Ala His Asn Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu	
190 195 200	
cac tgc cag agg gtg ccc tcg gcc agg ccc gtc ccc cag cca ccc ccc	675
His Cys Gln Arg Val Pro Ser Ala Arg Pro Val Pro Gln Pro Pro Pro	
205 210 215	
gct gcc ccg ccc cgg gtc tac caa cca ccc acc tac aac cgc atc atc	723
Ala Ala Pro Pro Arg Val Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile	
220 225 230	
aac cag atc tct acc aac gag atc cag agt gac cag aac ctg aag gtg	771
Asn Gln Ile Ser Thr Asn Glu Ile Gln Ser Asp Gln Asn Leu Lys Val	
235 240 245 250	
ctg cca ccc cct ctg ccc act atg ccc act ctc acc agc ctc cca tct	819
Leu Pro Pro Pro Leu Pro Thr Met Pro Thr Leu Thr Ser Leu Pro Ser	

49321-142 SEQ LIST.txt

255	260	265	
tcc acc gac aag ccg tcg ggc cca tgg aga gac tgc ctg cag gcc ctg Ser Thr Asp Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu 270 275 280			867
gag gat ggc cac gac acc agc tcc atc tac ctg gtg aag ccg gag aac Glu Asp Gly His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn 285 290 295			915
acc aac cgc ctc atg cag gtg tgg tgc gac cag aga cac gac ccc ggg Thr Asn Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly 300 305 310			963
ggc tgg acc gtc atc cag aga cgc ctg gat ggc tct gtt aac ttc ttc Gly Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe 315 320 325 330			1011
agg aac tgg gag acg tac aag caa ggg ttt ggg aac att gat ggc gaa Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu 335 340 345			1059
tac tgg ctg ggc ctg gag aac att tac tgg ctg acg aac caa ggc aac Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn 350 355 360			1107
tac aaa ctc ctg gtg acc atg gag gac tgg tcc ggc cgc aaa gtc ttt Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe 365 370 375			1155
gca gaa tac gcc agt ttc cgc ctg gaa cct gag agc gag tat tat aag Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys 380 385 390			1203
ctg cgg ctg ggg cgc tac cat ggc aat gcg ggt gac tcc ttt aca tgg Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp 395 400 405 410			1251
cac aac ggc aag cag ttc acc acc ctg gac aga gat cat gat gtc tac His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr 415 420 425			1299
aca gga aac tgt gcc cac tac cag aag gga ggc tgg tgg tat aac gcc Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala 430 435 440			1347
tgt gcc cac tcc aac ctc aac ggg gtc tgg tac cgc ggg ggc cat tac Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr 445 450 455			1395
cgg agc cgc tac cag gac gga gtc tac tgg gct gag ttc cga gga ggc Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly 460 465 470			1443
tct tac tca ctc aag aaa gtg gtg atg atg atc cga ccg aac ccc aac Ser Tyr Ser Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn 475 480 485 490			1491
acc ttc cac taa gccagctccc cctcc			1518

49321-142 SEQ LIST.txt

Thr Phe His

<210> 30
 <211> 493
 <212> PRT
 <213> Homo sapiens

<400> 30

Met Arg Pro Leu Cys Val Thr Cys Trp Trp Leu Gly Leu Leu Ala Ala
 1 5 10 15

Met Gly Ala Val Ala Gly Gln Glu Asp Gly Phe Glu Gly Thr Glu Glu
 20 25 30

Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn Arg Tyr Lys Arg Ala Gly
 35 40 45

Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe Ile Val Pro Gln Gln Arg
 50 55 60

Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu Pro Glu Val Leu Leu
 65 70 75 80

Glu Asn Arg Val His Lys Gln Glu Leu Glu Leu Leu Asn Asn Glu Leu
 85 90 95

Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu Gln Gln Leu Val Glu Val
 100 105 110

Asp Gly Gly Ile Val Ser Glu Val Lys Leu Leu Arg Lys Glu Ser Arg
 115 120 125

Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu
 130 135 140

Ile Ile Arg Lys Arg Asp Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn
 145 150 155 160

Arg Ile Leu Asn Gln Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr
 165 170 175

Lys Asp Leu Glu His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn
 180 185 190

49321-142 SEQ LIST.txt

Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro
 195 200 205

 Ser Ala Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val
 210 215 220

 Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
 225 230 235 240

 Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu Pro
 245 250 255

 Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys Pro Ser
 260 265 270

 Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly His Asp Thr
 275 280 285

 Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg Leu Met Gln
 290 295 300

 Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln
 305 310 315 320

 Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr
 325 330 335

 Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu
 340 345 350

 Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr
 355 360 365

 Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe
 370 375 380

 Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr
 385 390 395 400

 His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe
 405 410 415

 Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His
 420 425 430

49321-142 SEQ LIST.txt

Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
 435 440 445

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp
 450 455 460

Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
 465 470 475 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
 485 490

<210> 31
 <211> 25
 <212> DNA
 <213> artificial sequence

<220>
 <223> LOX-specific PMO antisense oligonucleotide

<400> 31
 ggagcacggt ccaggcgaag cgcacat 25

<210> 32
 <211> 25
 <212> DNA
 <213> artificial sequence

<220>
 <223> NOV-specific PMO antisense oligonucleotide

<400> 32
 agctcgtgct ctgcacactc tgcacat 25

<210> 33
 <211> 25
 <212> DNA
 <213> artificial sequence

<220>
 <223> ANGPTL2-specific PMO antisense oligonucleotide

<400> 33
 agcatgtcac gcacagtggc ctcacat 25